

GenCore version 4.5
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Run on: May 22, 2002, 15:04:28 ; Search time 55.81 Seconds

772.203 Million cell updates/sec

Title:	US-09-596-196-4
Perfect score:	3104

Sequence: 1 MMSPSQASLLFLNVCIFCG.....PVKIKSVSMKIRRMNPNPYEK 388

Scoring table: BLOSUM62

Searched: 747574 seqs, 111073796 residues

total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

FILE COPY

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2104	100.0	388	22	AAB82584	Human prothrombin
2	2100	99.8	388	22	AAV72622	Human prothrombin
3	2000	95.1	368	22	AAB82585	Human prothrombin
4	1729	82.2	326	22	AAU14275	Human novel prote
5	1729	82.2	326	22	AAU14511	Human novel prote
6	1729	82.2	326	22	AAB82590	Human prothrombin
7	1625	77.2	306	22	AAB82593	Human prothrombin
8	1299	61.7	237	22	AAB82592	Human prothrombin
9	1265	60.1	240	22	AAB82592	Human prothrombin
10	634	30.1	141	22	ABG23365	Human prothrombin
11	628.5	29.9	138	22	ABG23361	Human prothrombin

[illegible]

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CC The present invention relates to human **angiotensin polypeptides** such
 CC as CG006, CG007, CG015, CG14 and CG25. **The angiotensin polypeptides**
 CC are used as hybridisation probes, for chromosome and gene mapping, to
 CC identify polymorphism and for recombinant protein production.
 CC Angiotensin may be useful for modulating vascular stability and
 CC neovascularisation associated with various pathologies. It is used as a
 CC nutritional supplement, molecular weight marker and in gene therapy. It
 CC is also used for preventing, treating or ameliorating angiogenesis
 CC related disorders such as myocardial infarction, proliferative
 CC retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia,
 CC bone disorders (e.g., osteoporosis), abnormal vascular growth, cancer,
 CC anaemia and chronic inflammation (e.g., asthma and arthritis) and immune
 CC disorders (e.g., inflammatory reactions and autoimmune diseases).
 CC haematopoiesis related disorders (e.g., myeloid or lymphoid cell
 CC deficiencies), coagulation disorders, leukaemia and nervous system
 CC disorders. It is also used in drug screening techniques for screening
 CC compounds which are able to modulate the expression or activity of
 CC angiotensin. The compounds can also be used to treat diseases and
 CC disorders.

Sequence 388 AA:

Query Match Score 2100; DB 22; Length 388;
 Best Local Similarity 99.8%; Pred. No. 1.8e-204;
 Matches 387; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMSPSQSLFLVNCIFGEGVQNCVHSTDSVYVIVEDGSNAKDESKNDYVCKED 60
 DB 1 mmspsqasllflnvcilfgegvqncvhsstsvvivedgsnadeskndetcked 60
 QY 61 CEESDVKTKITREEKHEKRNLSIVSTYSTRKLLRNMDQOASLDYLSNOVNEIM 120
 DB 61 ceesdvkktitreekhekrnlisvststrkllrnmdeqasldylsnvneim 120
 QY 121 NRVLTLTEVERKQDLPFHPVQSHGLDCTDIKDTIGSVTKPSGLYIIHPEGSSYPE 180
 DB 121 nrvlltteverfkqldpfhprvqshgldctdiktigsvtkpsgylaihpegssype 180
 QY 121 nrvlltteverfkqldpfhprvqshgldctdiktigsvtkpsgylaihpegssype 180
 QY 181 VACDMDYRGGWTVIQKRIDGIIDPQRLWCYLDLGFGLLGEFWLGLKRIEYVNOKNTS 240
 DB 181 vmcdmdyrggwvtvqkrldgidpqrllwcyldlfgfllgefwlglkrieyvnoqnts 240
 QY 241 FMYLVALESEDDTLAYASVNDNFLEDERFEKMHIGRYSGNAGDAFRGLKEDNNAPE 300
 DB 241 fmylvaaleseddtlayasvndnflwedrfekmhigrysnagdafrglkednnapf 300
 QY 301 STSDVNDGCRPACLVNGSVKSCSHLNKGTGMFNECGLANLNGIHHSGLATG10W 360
 DB 301 stsdvndgcrpactlvngsvskshlnkgtgmfnecglanlngihhsfslatg1qW 360
 QY 361 GTWTKNNSPVKIKSVSMKIRMYNPFK 388
 DB 361 gtwtknnsprvkiksvsmkirmynpfk 388
 QY 361 gtwtknnsprvkiksvsmkirmynpfk 388

RESULT 3

AAB82589 ID AAB82589 standard; Protein; 368 AA.

XX AC AAB82589;

DT 02-OCT-2001 (first entry)

DE Human prothrombinase-like polypeptide (mature protein).

XX Prothrombinase-like polypeptide: human; haemostatic; coagulant;

KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytosolic;

KW antitartaric; antileukemic; antineurotic; osteoporosis;

KW immunomodulatory; antineumatic; antitartaric; antineurotic;

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 161..197
 FT Domain /note="fibrinogen beta/gamma chain"
 FT Domain 202..214
 FT Domain /note="fibrinogen beta/gamma chain"
 FT Domain 251..265
 FT Domain /note="fibrinogen beta/gamma chain"
 FT Domain 304..333
 FT Domain /note="fibrinogen beta/gamma chain"

W020153456-A2.

26-JUL-2001.

22-DEC-2000; 2000WO-US35061.

21-JAN-2000; 2000US-0488725.

25-JAN-2000; 2000US-0491404.

25-APR-2000; 2000US-0552317.

17-JUN-2000; 2000US-0596196.

31-AUG-2000; 2000US-0643313.

(HSE-) HSEQ INC.

Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;

Arterburn MC, Tang YT, Liu C, Drmanac R;

WPI: 2001-483140/52.

N-PSDB; AAH26235; AAH26236.

Claim 10; Page 128-129; 140pp; English.

The present sequence is that of human secreted prothrombinase-like polypeptide (PLP) mature polypeptide, as predicted from polynucleotides (see AAH26235-36) derived from an ovary cDNA clone. PLP polynucleotides and polypeptides, including the mature protein, can be used in the diagnosis, treatment and/or prevention of diseases associated with the dysregulation of coagulation pathways, such as haemophilia, myocardial infarction, glomerular disease, diabetes, fulminant viral hepatitis and atherosclerosis. They may also be beneficial in the treatment of viral infections and some forms of cancer. A claimed method of treating a subject in need of enhanced PLP activity or expression involves the administration of PLP, a PLP agonist or a polynucleotide encoding PLP. A claimed method of treating a subject having need to inhibit activity or expression of PLP involves the administration of a PLP antagonist, a polynucleotide that inhibits expression of a PLP polynucleotide, or a polypeptide that competes with the PLP for its ligand. The polypeptides can also be used to raise antibodies, as food supplements, and to screen for agonists and antagonists.

Sequence 368 AA:

Query Match Score 2000; DB 22; Length 368;
 Best Local Similarity 100.0%; Pred. No. 2.4e-194;
 Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 EVVQNCVHSTDSVYVIVEDGSNAKDESKNDYVCKEDSCDKTKITREEKHEK 80
 DB 1 evvgncvhsstdsyvviwedgsnadeskndetckedcdkktitreekhmc 60
 QY 81 RNLSNIVSYSTRKLLRNMDQOASLDYLSNOVNEIMRVLLTTEVFRKQDLPFPH 140
 DB 61 rnlsvsystrkllrnmdeqasldylsnvneimrvllttevfrqldpfph 120
 QY 141 RPVQSHLDCDCTDIKDTIGSVTKPSGLYIIHPEGSSYPEVWCDMDYRGGWTVIOKRID 200
 DB 121 rpvqshldctdiktigsvtktpsglyaihpegssypfewcdmdyrggwvtvirkid 180

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:05:08 ; Search time 22.62 Seconds
(without alignments)
418.971 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104

Sequence: 1 MMSPSQASLFLANVICFIG.....PVKIKSVSMKIRMYNPFYK 388

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Optimal number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
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3: /cgnt2_6/prodata/2/1aa/5A_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	20.2	491	2	US-08-933-821-4
2	425	20.2	491	3	US-08-960-507-4
3	425	20.2	491	4	US-09-136-828-4
4	405.5	19.3	480	4	US-08-740-223A-12
5	403.5	19.2	487	4	US-08-740-223A-4
6	402.5	19.1	497	1	US-08-373-579-4
7	402.5	19.1	497	2	US-08-418-595-4
8	402.5	19.1	497	2	US-08-665-926-4
9	402.5	19.1	497	2	US-08-348-492-4
10	402.5	19.1	497	2	US-09-162-437-4
11	400	19.0	493	2	US-08-933-821-2
12	400	19.0	493	3	US-08-960-507-2
13	400	19.0	493	3	US-09-136-828-2
14	399	19.0	493	1	US-08-525-505A-4
15	395.5	18.8	486	4	US-08-740-223A-22
16	395	18.8	478	4	US-08-740-223A-7
17	395	18.8	495	4	US-08-740-223A-26
18	395	18.8	498	4	US-08-740-223A-2
19	395	18.8	498	4	US-09-351-457-2
20	395	18.8	498	4	US-09-561-500-2
21	395	18.8	498	4	US-09-561-108-2
22	394	18.7	495	4	US-09-351-457-5
23	394	18.7	495	4	US-09-351-500-5
24	394	18.7	495	4	US-09-561-108-5
25	393	18.7	491	4	US-08-740-223A-13
26	389	18.5	314	1	US-08-525-505A-2
27	389	18.5	498	1	US-08-373-579-2

28	389	18.5	498	2	US-08-418-595-2	Sequence 2, Appl
29	389	18.5	498	2	US-08-665-926-2	Sequence 2, Appl
30	389	18.5	498	2	US-08-348-492-2	Sequence 2, Appl
31	389	18.5	498	4	US-09-162-437-2	Sequence 2, Appl
32	387.5	18.4	497	4	US-08-740-223A-14	Sequence 14, Appl
33	381.5	18.1	480	4	US-08-373-579-6	Sequence 6, Appl
34	381.5	18.1	496	1	US-08-418-595-6	Sequence 6, Appl
35	381.5	18.1	496	2	US-08-665-926-6	Sequence 6, Appl
36	381.5	18.1	496	2	US-09-162-437-6	Sequence 6, Appl
37	381.5	18.1	496	4	US-08-740-223A-6	Sequence 6, Appl
38	381.5	18.1	496	4	US-09-351-457-4	Sequence 4, Appl
39	381.5	18.1	496	4	US-09-561-500-4	Sequence 4, Appl
40	381.5	18.1	496	4	US-09-561-108-4	Sequence 4, Appl
41	381.5	18.1	496	4	US-08-740-223A-24	Sequence 24, Appl
42	381.5	18.1	499	4	US-08-960-507-19	Sequence 19, Appl
43	381	18.1	346	3	US-08-206-176-4	Sequence 4, Appl
44	380	18.1	491	1		
45	375.5	17.8				

ALIGNMENTS

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RESULT 1
US-08-933-821-4
Sequence 4, Application US/08933821
Patent No: 5972328
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: The Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipat (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,821
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dregger, Ginger R.
REGISTRATION NUMBER: 33,055
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-933-821-4
Query Match 20.2%; Score 425; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 1e-35;
Matches 119; Conservative 64; Mismatched 133; Indels 126; Gaps 14;
QY 44 SNADEKSDNYCKECSQDYKITE-EKHFRCRLQNSIYSTSTKRLRNMM 102
Db 68 TRGDASTIDMTIRMLENLKDLISROKREIDVLQVVDGNIYNEVLLKRSNNM 127
QY 103 DE-QQASLDLY-----SNQVNEIDMNVLLITTE----- 129

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Db 128 SRVQLYMLLHEIRKRDNSLELSOLENKLINVTTEMLKMATRYRELEVKYASLTDLVN 187
Qy 130 -----VFRQ---LDP-----FPHRPVOSHGL----- 148
Db 188 NOSVMTLLEBQCLIFRSQDTHVSPLVQVPPHIPSQOYTPBLGNETIORDPGYPR 247
Qy 149 DCTDIDKDTIGSYTKTP-----SGLYIHPEGSSYPREV 181
Db 248 DLMPPDLATSPTKSPFKIPPYTFINEGPFKDCQAKGASHSVSGIYMIKIPENSNGPMQL 307
Qy 182 MCDMDYRGSGWTIVOKRIIDIFORLWCDYLDGFGDLGFEWGLKRIIFYIVNOKNTSF 241
Db 308 WCNESLDPGGWTIVOKRIDGVSYNFRNMENYKKGNGIDGFWLGLENIYMLSNODN--Y 365
Qy 242 MLYVALESDDTLAYASYDNFWLEDETRFFKMHGIRYSGNAGDAFRGLKREDNONAMPES 301
Db 366 KLIIELEDMDSKRYAAYESSFRLEPESEFYRLGLGYGNAGDSMMW-----HNGKQFT 419
Qy 302 TSDVDNDCRPACLVNGQSVKCSHLNKTGMWNECGLANGLIHHSKLLA---TGI 358
Db 420 TLDNRKD-----MYAGNCAHFH-KGGWYNACAHSLNGLVWYRGHYRSKHODGI 468
Qy 359 QMGWTKNNSPVKIKSVSMKIR 380
Db 469 FWAEX--RGGSYSLRAVQOMIK 488

RESULT 2
US-08-960-507-4
Sequence 4, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-960-507-4

Query Match 20.2%; Score 425; DB 3; Length 491;
Local Similarity 26.9%; Pred. No. 1e-35;
Conservative 64; Mismatches 133; Indels 126; Gaps 14;

Db 68 TKGQASTIKDMITRMADLENLKDVLRSROKREIDVLQVVDGNIYNEVKLRKESRMNN 127
Qy 103 DE-QQASLDYL-----SNQVNEIMNRVLLTTE----- 129
Db 128 SRVQLYMLLHEIRKRDNSLELSOLENKLINVTTEMLKMATRYRELEVKYASLTDLVN 187
Qy 130 -----VFRQ---LDP-----FPHRPVOSHGL----- 148
Db 188 NOSVMTLLEBQCLIFRSQDTHVSPLVQVPPHIPSQOYTPBLGNETIORDPGYPR 247
Qy 149 DCTDIDKDTIGSYTKTP-----SGLYIHPEGSSYPREV 181
Db 248 DLMPPDLATSPTKSPFKIPPYTFINEGPFKDCQAKGASHSVSGIYMIKIPENSNGPMQL 307
Qy 182 MCDMDYRGSGWTIVOKRIIDIFORLWCDYLDGFGDLGFEWGLKRIIFYIVNOKNTSF 241
Db 308 WCNESLDPGGWTIVOKRIDGVSYNFRNMENYKKGNGIDGFWLGLENIYMLSNODN--Y 365
Qy 242 MLYVALESDDTLAYASYDNFWLEDETRFFKMHGIRYSGNAGDAFRGLKREDNONAMPES 301
Db 366 KLIIELEDMDSKRYAAYESSFRLEPESEFYRLGLGYGNAGDSMMW-----HNGKQFT 419
Qy 302 TSDVDNDCRPACLVNGQSVKCSHLNKTGMWNECGLANGLIHHSKLLA---TGI 358
Db 420 TLDNRKD-----MYAGNCAHFH-KGGWYNACAHSLNGLVWYRGHYRSKHODGI 468
Qy 359 QMGWTKNNSPVKIKSVSMKIR 380
Db 469 FWAEX--RGGSYSLRAVQOMIK 488

RESULT 3
US-09-136-828-4
Sequence 4, Application US/09136828
Patent No. 6350450
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,828
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130R1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-828-4

Query Match 20.2%; Score 425; DB 4; Length 491;
Best Local Similarity 26.9%; Pred. No. 1e-35;

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:13:50 ; Search time 17.4 Seconds
(without alignments)
818.896 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000
Sequence: 1 EYVQGNCHVHSTDSYVNVY.....PVKIKSVSMKIRRNYPFK 368

Scoring table: BLOSUM62
Gapop: 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SWISSProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	20.7	439	1	FGI2_HUMAN
2	405.5	20.3	432	1	FGI2_MOUSE
3	400.5	20.0	481	1	AGP1_BOVIN
4	400.5	20.0	493	1	ANL2_MOUSE
5	400.0	20.0	493	1	ANL2_HUMAN
6	398.0	19.9	432	1	FGI2_HUMAN
7	395.5	19.8	468	1	FGI2_BOVIN
8	395.0	19.8	498	1	AGP1_HUMAN
9	391.0	19.6	498	1	AGP1_MOUSE
10	381.5	19.1	496	1	AGP2_HUMAN
11	375.5	18.8	491	1	FIBB_HUMAN
12	375.0	18.8	375	1	AGP2_BOVIN
13	374.5	18.7	479	1	AGP2_MOUSE
14	373.5	18.7	479	1	FIBB_RAT
15	371.5	18.5	463	1	FIBB_CHICK
16	370.0	18.5	477	1	FIBB_PETMA
17	367.5	18.4	453	1	FIBG_HUMAN
18	365.0	18.2	444	1	FIBG_BOVIN
19	360.0	18.0	432	1	FIBG_PETMA
20	358.0	17.9	509	1	AGP4_MOUSE
21	358.0	17.9	503	1	AGP4_HUMAN
22	352.5	17.6	438	1	FIBG_XENLA
23	351.0	17.5	319	1	FCN2_RAT
24	350.5	17.5	282	1	FIBB_PARPA
25	348.5	17.4	774	1	SCA_DROME
26	347.5	16.9	866	1	FIBA_HUMAN
27	335.5	16.8	741	1	FIBA_CHICK
28	332.0	16.6	306	1	FCN2_MOUSE
29	329.5	16.5	641	1	FIB2_PETMA
30	329.0	16.4	334	1	FCN1_MOUSE
31	327.5	16.4	445	1	FIBG_RAT
32	321.5	16.1	313	1	FCN2_HUMAN
33	321.0	16.1	255	1	MEF4_HUMAN

34	313.5	15.7	782	1	FIBA_RAT	P06399 rattus norv
35	310.5	15.5	1808	1	TENA_CHICK	P10039 gallus gall
36	305.5	15.3	335	1	FCN1_RAT	Q9WCS8 rattus norv
37	303.5	15.2	326	1	FCN1_HUMAN	O00602 homo sapien
38	302.5	15.1	4289	1	TENX_HUMAN	P22105 homo sapien
39	291.0	14.6	299	1	FCN3_HUMAN	O73636 homo sapien
40	282.5	14.1	1746	1	TENA_PIG	O29116 sus scrofa
41	271.0	13.6	2201	1	TENA_HUMAN	P24821 homo sapien
42	197.0	9.8	137	1	AGP2_RAT	O35462 rattus norv
43	109.0	5.5	129	1	MEF4_BOVIN	P55918 bos taurus
44	98.0	4.9	782	1	BICD_DROME	P16568 drosophila
45	97.5	4.9	1432	1	SKI3_YEAST	P17883 saccharomyc

ALIGNMENTS

RESULT 1
FGI2_HUMAN STANDARD: PRT: 439 AA.
ID FGI2_HUMAN
AC 014314;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibrinogen precursor (Fibrinogen-like protein 2) (P1949).
GN Fgi2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pytela R.;
RT *Sequence of a human transcript expressed in T-lymphocytes and
RT encoding a fibrinogen-like protein.";
RL Gene 160:257-262(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Yumazaki S., Liu M., Marsden P., Jevy G.
RT Submitting and characterizing a cDNA for the human source of the
RT mouse gene Fgi2.
RL Submitted (NOV-1998) to the EMBL/Genbank/DBI databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98309432; PubMed=9647217;
RA Marzetti S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA Argaves S., von Fiedner V., Pytela R., Ruegg C.;
RT *Characterization of human fibrinogen, a fibrinogen-like protein
RT secreted by T lymphocytes.";
RL J. Immunol. 161:138-147(1998).
RN [4]
RP FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
RN MUCOSAL SITES.
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
DR EMBL: Z36531; CAAB5298.1;
DR EMBL: AF104015; AAD10825.1;
DR EMBL: AF104014; AAD10825.1; JOINED.
DR HSSP: P02671; 1FZD.
DR MIM: 605351; -.

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DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FBG.1.
 DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
 KW T-cell; glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 439
 FT DOMAIN 210 435
 FT DISULFID 213 242
 FT DISULFID 371 384
 FT CARBOHYD 25 25
 FT CARBOHYD 179 179
 FT CARBOHYD 235 235
 FT CARBOHYD 263 263
 FT CARBOHYD 336 336
 SO SEQUENCE 439 AA; 50228 MW; DF34656288E49E68 CRC64;

Query Match 20:308 Score 413.5; DB 1; Length 439;
 Local Similarity 30:298 Pred. No. 8.6e-26;
 Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

QY 14 SSVAVIVEDDSNAKDESKNDYCKEDCE-----ESCQVYTK 50
 DB 73 SRIEVEKEVQNKKEIVNSLKKSC-QDCKLQADDNDGPRNGLLPSTGAPGEVGDNRVR 131
 QY 51 ITREKHFMCNLONS-IVSYRSTKLLRNM-MDEQASLDYLSNQVELM 100
 DB 132 ELSEVVKLSSELKNKEIVNLHGRLEKLNVMNNIENVDSKANLFPVNSLDGKC 191
 QY 101 NRVLTLTEVFRKQDLPFPRPVSHGL--DCTDIKDTIGSVTKPSGLYIIEHSSYP 158
 DB 192 SKC-----PSEQIQSRPVQ-HLTKDCSDY--AIGRSSSTYKVPDPKNS 237
 QY 159 FEVACDMDYRGGWTVYQKRIIDQRLMCDLIDGFDLGFVGLKFIYVNOKN 218
 DB 238 FEVACDMDYRGGWTVYQKRIIDQRLMCDLIDGFDLGFVGLKFIYVNOKN 218
 QY 219 TSFMYALVASEDDTLVASYDNFMLEDETFPFKMLHGRYSGNAGDAFRGLKEDNONAM 278
 DB 296 KEMIRIDLEDFNGVELYALDOFYVANEFLKRLHVGNYGTGADALR-FNKHYNHDLK 354
 QY 279 PFSTSDVNDGCRPACLVNGOSVKSCHLNKKTGWMEGCLANLNG-IHFSGLKLTATG 337
 DB 355 FEFTPPDKNDRYPSG-----NCG-LYSSGWMFPACLSANLNGKYVHQKRYGVANG 404
 QY 338 IOWGTW--TKNNSPYKIKSVSMKIRRMVNP-YFK 368
 DB 405 IFWGTWPGVSEAHGPGYKRSFKAKMIRPKHF 438

RESULT 2
 FGL2_MOUSE STANDARD; PRI; 432 AA.
 ID FGL2_MOUSE
 AC 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrinogen precursor (Fibrinogen-like protein 2) (Prothrombinase)
 DE (Cytotoxic T-lymphocyte specific protein).
 GN FGL2 OR FIBLP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI-TaxID:10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE-Cytotoxic T-cell;
 RX MEDLINE=87175527; PubMed=3550794;
 RA Koyama T., Hall L.R., Haser W.G., Tonegawa S., Salto H.;
 RT Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
 RT homology to fibrinogen beta and gamma chains;
 RT Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).

RN [2]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RC STRAIN-BALB/CJ; TISSUE-Peritoneal macrophage;
 RX MEDLINE=95333285; PubMed=7609073;
 RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
 RA Levy G.;
 RT virus-induced prothrombinase activity."
 RL J. Virol. 69:5033-5038(1995).
 CC -1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
 CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
 CC T-CELLS.
 CC -1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
 CC VIRUS STRAIN 3 (MHV-3).
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).

CC EMBL: M16238; AAA37624.1;
 CC EMBL: M15761; AAA37624.1; JOINED.
 CC EMBL: S78773; AAB34823.1;
 CC PIR: A27447; A27447.
 CC HSP: P02671; 1FZD.
 CC MGD: MGI:103266; Fgl2.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FBG.1.
 DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
 KW T-cell; Cytolysis; Signal.
 FT SIGNAL 19
 FT CHAIN 20 432
 FT DOMAIN 203 428
 FT DISULFID 206 235
 FT DISULFID 364 377
 FT CARBOHYD 24 24
 FT CARBOHYD 172 172
 FT CARBOHYD 228 228
 FT CARBOHYD 256 256
 FT CARBOHYD 329 329
 FT CONFLICT 332 332
 FT SEQUENCE 432 AA; 48951 MW; 2B297F69CBA4A782 CRC64;

Query Match 20:380 Score 405.5; DB 1; Length 432;
 Local Similarity 35:408 Pred. No. 3.7e-25;
 Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 78 LRNMDEQA-----SLDYLSNQVELMNRVLLLTTEVFRKQD-----PFP 119
 DB 137 LKNARDQIQGLQGRLETLALVNMNNIENVYDNKANLTVV--NSLDGSKSCPSQEMQ 194
 QY 120 HRPVQSHGL--DCTDIKDTIGSVTKPSGLYIIEHSSYPFEVACDMDYRGGWTVYQK 177
 DB 195 SOPVQ-HLTKDCSD-HYVLG---RRSGATRVDPDHNSSEFYVCOMETGGGWTVYQA 249
 QY 178 RIDGIIDPQRLMCDYLDGFDLGFVGLKFIYVNOKNTSEMLYALVASEDDTLAYA 237
 DB 250 RIDGSTNFTREKWDYKAGFNLEREFVGLGNDKIHLLT--KSEKEMIRIDLEDFNGLTLYA 307
 QY 238 SYDNFMLEDETFPFKMLHGRYSGNAGDAFRGLKEDNONAMPSTSDVNDGCRPACLVN 297
 DB 308 LYDOFYVANEFLKRLHVGNYGTGADALR-FSRHYNDLRFETPPDNDNRYSG----- 362
 QY 298 GGSVKSCHLNKKTGWMEGCLANLNG-IHFSGLKLTATGIOWGTWTKNN--SPVKIKS 354

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22-DEC-2000; 2000WO-US35061.

PR 21-JAN-2000; 2000US-0488725.
PR 25-JAN-2000; 2000US-0491404.
PR 25-APR-2000; 2000US-0552317.
PR 17-JUN-2000; 2000US-0596196.
PR 31-AUG-2000; 2000US-0643313.
XX
XX
XX (HYSE-) HYSEQ INC.
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX WPI: 2001-483140/52.
DR N-PSDB; AAH26235, AAH26236.
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX
PS Claim 10; Page 128-129; 140pp; English.
XX
CC The present sequence is that of human secreted prothrombinase-like
CC polypeptide (PLP) mature polypeptide, as predicted from
CC polynucleotides (see AAH26235-36) derived from an ovary cDNA clone.
CC PLP polynucleotides and polypeptides, including the mature protein,
CC can be used in the diagnosis, treatment and/or prevention of diseases
CC associated with the dysregulation of coagulation pathways, such as
CC haemophilia, myocardial infarction, glomerular disease, diabetes,
CC fulminant viral hepatitis and atherosclerosis. They may also be
CC beneficial in the treatment of viral infections and some forms of
CC cancer. A claimed method of treating a subject in need of enhanced
CC PLP activity or expression involves the administration of PLP, a
CC PLP agonist or a polynucleotide encoding PLP. A claimed method of
CC treating a subject having need to inhibit activity or expression of
CC PLP involves the administration of a PLP antagonist, a
CC polynucleotide that inhibits expression of a PLP polynucleotide,
CC or a polypeptide that competes with the PLP for its ligand. The
CC polypeptides can also be used to raise antibodies, as food
CC supplements, and to screen for agonists and antagonists.
XX
XX Sequence 368 AA;

Query Match 100.0%; Score 2000; DB 22; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.6e-195;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYVQNCVHHSTDDSVNIVEDGSNAKDESKNDTVCKEDCESDVKTITREKHEMC 60
DB 1 EVVQNCVHHSTDDSVNIVEDGSNAKDESKNDTVCKEDCESDVKTITREKHEMC 60
QY 61 RNLONSIVSYRSTKLLRNMMDEQASLDYLSNOVNELMNVLLLTPEVFKOLDPPH 120
DB 61 RNLONSIVSYRSTKLLRNMMDEQASLDYLSNOVNELMNVLLLTPEVFKOLDPPH 120
QY 121 RPYVSHGLDCTDIDKDTISVTKTPSGLYIIHPEGSSYPFEVACDMYRGGCTVIQKRID 180
DB 121 RPYVSHGLDCTDIDKDTISVTKTPSGLYIIHPEGSSYPFEVACDMYRGGCTVIQKRID 180
QY 181 GIIDPQRLMCOYLDGFGDGLGEFWLGLKKIYIVNQKNTSEMLVYALASEDDTLAYASYD 240
DB 181 GIIDPQRLMCOYLDGFGDGLGEFWLGLKKIYIVNQKNTSEMLVYALASEDDTLAYASYD 240
QY 241 NFWLEDERFPFMHLGRYSGNAGDAFRGLKKEDNONAMPFSRSDVDNCCRACLVNQS 300
DB 241 NFWLEDERFPFMHLGRYSGNAGDAFRGLKKEDNONAMPFSRSDVDNCCRACLVNQS 300
QY 301 VKSCSHLHNTGWMENECGLANLNGIIHPSGKLATGIQWGTWTKNNSPVKIKTSVMKIR 360
DB 301 VKSCSHLHNTGWMENECGLANLNGIIHPSGKLATGIQWGTWTKNNSPVKIKTSVMKIR 360
QY 361 RMYNDYEF 368
DB 361 RMYNDYEF 368

RESULT 2
AAB82584
ID AAB82584 standard; Protein; 388 AA.
XX
AC AAB82584;
XX
XX 02-OCT-2001 (first entry)
DE Human prothrombinase-like polypeptide.
XX
XX Prothrombinase-like polypeptide; human; haemostatic; cardiant;
KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW antiarteriosclerotic; anticancer; vulnerrary; osteoporosis;
KW immunomodulatory; antineumalic; antiarthritic; antiinflammatory;
KW thrombolytic; diagnosis; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..20
FT /label= Signal_peptide
FT Protein 21..388
FT /label= Mature_protein
FT /note= "separately claimed in Claim 10"
FT Domain 181..217
FT /note= "fibrinogen beta/gamma chain"
FT /note= "separately claimed in Claim 10"
FT Domain 222..234
FT /note= "separately claimed in Claim 10"
FT Domain 271..285
FT /note= "fibrinogen beta/gamma chain"
FT /note= "separately claimed in Claim 10"
FT Domain 324..353
FT /note= "fibrinogen beta/gamma chain"
FT /note= "separately claimed in Claim 10"
XX
XX WO200153456-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35061.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-JAN-2000; 2000US-0491404.
XX 25-APR-2000; 2000US-0552317.
XX 17-JUN-2000; 2000US-0596196.
XX 31-AUG-2000; 2000US-0643313.
XX
XX (HYSE-) HYSEQ INC.
PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
XX WPI: 2001-483140/52.
DR N-PSDB; AAH26235, AAH26236.
PT Novel prothrombinase-like polypeptides and polynucleotides useful in
PT diagnosing and treating e.g. myocardial infarction and diabetes -
XX
XX Claim 10; Page 126-127; 140pp; English.
XX
XX The present sequence is that of a novel human secreted
CC prothrombinase-like polypeptide (PLP). The polypeptide has a
CC predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid
CC sequence similarity to human prothrombinase Fg12 protein. The
CC sequence was predicted from polynucleotides (see AAH26235-36)
CC derived from a human ovary cDNA clone. PLP polynucleotides and
CC polypeptides, including the mature protein, polypeptides including
CC PLP fibrinogen chains, and a soluble splice variant (see AAB82590),
CC can be used in the diagnosis, treatment and/or prevention of diseases
CC associated with the dysregulation of coagulation pathways, such as

QY	181	GIIDFQRIKMCYLDLFGDGLGEEFNLGLKRTFYLYNQKNTSPMLVVALESDDTLATASYD	240
Db	201	glddfrtwcdyldgfgdliqefwlgiklftfyngkntsfmlyvalasedtlayasyd	260
QY	241	NFWLEDETRFFKMLGRSGNAGAPFGLKKEQNQNPSTSPVDNDGCRPACLVNGOS	300
Db	261	nfwledetrffkmlhgrysngagafgylkkehqnmprfstadvndgcrpactlvngqs	320
QY	301	VKSCSHLNKTKGMWPFNECGLANLNGIHNFSGKLLATSIQMGWTMKNNSPVKISYSMKIR	360
Db	321	vkscshlnhktcgwwfnecglaanlghfsgagllatqlygwctwcknspkiksvsmkirk	380
QY	361	RMVNPYFK 368	
Db	381	rmynpyik 388	
AA82593	4		
ID	AA82593	standard; Protein: 306 AA.	
AC	AA82593:		
DT	02-OCT-2001	(first entry)	
XX		Human prothrombinase-like polypeptide splice variant mature protein.	
DE		Prothrombinase-like polypeptide; human; haemostatic; cardiac; nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic; antiatherosclerotic; antitumor; vulnerary; osteoporosis; immunomodulatory; antirheumatic; antiarthritic; antiinflammatory; thrombolytic; diagnosis; therapy.	
XX			
OS		Homo sapiens.	
XX			
PN	MO200153456-A2.		
PD	26-JUL-2001.		
XX			
PF	22-DEC-2000; 2000MO-US35061.		
XX			
PR	21-JAN-2000; 2000US-0488725.		
PR	25-JAN-2000; 2000US-0491404.		
PR	17-JUN-2000; 2000US-0552317.		
PR	15-APR-2000; 2000US-0596196.		
PR	31-AUG-2000; 2000US-0643313.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C; Arterburn MC, Tang YT, Liu C, Drmanac R;		
XX			
DR	WPI: 2001-483140/52.		
XX	N-PSDB: AAH26237.		
XX			
PT	Novel prothrombinase-like polypeptides and polynucleotides useful in		
XX	diagnosing and treating e.g. myocardial infarction and diabetes -		
XX	Claim 10; Page 135-136; 140pp; English.		
XX			
CC	The present sequence is that of the mature portion of a novel		
CC	secreted, soluble splice variant (see AA82590) of novel human		
CC	prothrombinase-like polypeptide (PLP). PLP polynucleotides and		
CC	polypeptides, including those comprising the mature protein of the		
CC	PLP splice variant, can be used in the diagnosis, treatment and/or		
CC	prevention of diseases associated with the dysregulation of		
CC	coagulation pathways, such as haemophilia, myocardial infarction,		
CC	glomerular disease, diabetes, fulminant viral hepatitis and		
CC	atherosclerosis. They may also be beneficial in the treatment of		
CC	viral infections and some forms of cancer. A claimed method of		
CC	treating a subject in need of enhanced PLP activity or expression		
CC	involves the administration of PLP, a PLP agonist or a		

Query Match	81.2%	Score 1625	DB 22	Length 306
Best Local Similarity	83.2%	Pred. NO. 2.5e-157		
Matches 306	Conservative	0	Mismatches 0	Indels 62
			Gaps	
QY 1 EVVQNCVHNHSTDDSVYVNIVEDGSNAKDESKNDYTCEDCESECDYKTKITREKHFMC 60				
Db 1 evvgncvnhstddsvynlivedgsnakdeskandtyckedceescdvckkltreekhfmc 60				
QY 61 RNLQNSIVSYSTRSTKLLRNMMDEQASLDYISNOVNEMLNRVLLLTVEVFRKQDPRH 120				
Db 61 rnlqnsivsystrstckllrnmmdqgasldylsnqyneimnrvlllttevfekqldprfh 120				
QY 121 RVQSHGIDCTPTIKPTISVTKTPSGLYIINHEGSSYPRFEWCMQYRGGWYVIOKRID 180				
Db 121 rrvqshgidctptikptisvktprsglyiilnhegsysprfemcdmryrggwvtylqkrld 180				
QY 181 GIIDPRLMCDYLDLDFGDLDFGEFWMGLKRIFYVNQKNPSFMYALFESDDTLAAYSD 240				
Db 181 gildpfrlmcdyldldfgdlldfgefwmlgkriifyvnqknpsfmyalfesddtlaaysyd 240				
QY 241 NEWLEDETRFEFKMLGRYSGNAGDAFERGLKKEEDNONAMPSTSDVNDGCRPACLVNGOS 300				
Db 201 -----gdafgylkkedngnampfstadvndgcrpaelvngos 238				
QY 301 VKSCSHLHKKTGMWFMEECLANLNGIHNSGKLLAGIGIOWGTMTKNSPVKIKSVSMKTR 360				
Db 239 vkschshlhnkktgwmfwmeeglanlngihhtgskllacgylqwgvtcknspvklksvsmktr 298				
QY 361 RMYNPFYK 368				
Db 299 rmynpfyk 306				
RESULT 5				
AAU14275				
ID AAU14275 standard; Protein; 326 AA.				
XX AAU14275;				
XX				
DT 24-OCT-2001 (first entry)				
XX				
DE Human novel protein #146.				
XX				
KM Human; novel protein; Antianaemic; osteopathic; antiinflammatory;				
KM immunomodulatory; cyostatic; neuroprotective; vulnerrary; nootropic;				
KM anticovulsant; antiallergic; cerebroprotective; antifungal; antiviral;				
KM antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;				
KM thrombolytic; immunogen; antibody; gene therapy; neurological disorder;				
KM Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;				
KM tissue regeneration; immune disorder.				
XX				
OS Homo sapiens.				
PM WO200155437-A2.				
XX				
PD 02-AUG-2001.				
XX				
PF 25-JAN-2001; 2001WO-US02623.				
XX				
PR 25-JAN-2000; 2000US-0491404.				
XX				
PA (HYSEQ) HYSEQ INC.				

XX Tang YT, Liu C, Dirmanac RT;
 XX WPI: 2001-451939/48.
 XX DR N-PSDB; AAS22580.
 XX
 PT Isolated polypeptides useful for treating anti-inflammatory diseases
 PT nervous system disorders, and for regenerating bone and cartilage -
 XX
 PS Example 4; Page 605; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence represents a protein of the invention.

Sequence 326 AA:

Query Match	81.2%	Score 1625	DB 22	Length 326
Best Local Similarity	83.2%	Pred. No. 2.7e-157		
Matches 306	Conservative	0	Mismatches 0	Indels 62
				Gaps 1
QY	1	EVVQNCNVAHSTSDSSVYNIIVEDGSSNAKDESKNDYITCKEDCEESCQVKTITREEKHMC	60	
DB	21	evvgncnvhstsdssvyniivdgssnakdskndyitckedceescvktitreekhmc	80	
QY	61	RRLQNSIYSYRSTKLLRLNMMDBOQASLDYISNOVNEMLNRYLLITTEVFRKQDPPH	120	
DB	81	rrlqnsiysyrstskllrlnmmdboqasldyisnoynelmrnyllittevfrkqldpfbh	140	
QY	121	RPVQSHGDDCPTIKPTIGSVTKTPSGLYIITHPEGSSYPREVWCMDMYRCGGWTVIQKRD	180	
DB	141	rpvqshgddcctikptigsvtktpsglyiithpegssyplevwcmdmyrpggwvvlqkrid	200	
QY	181	GIIDFQRLMCDYLDLDFGDLGFEFWLGLKKIFVIYNOKNTSFMUYALBESDDTLAAYASYD	240	
DB	201	giidfgqrlmcdyldldfgdlgfefwlglkkifviynokntsfmuyalbesddtlaayasyd	220	
QY	241	NFWLEDETRFFFMHLGRYSGNAGDAFRGLKKEEDNQNAFPSTSDVNDGCRPACLVNGOS	300	
DB	221	nfwledeeffffmhlgrysgnagdafrglkkekdnqnafpstsdvndgcrpactlvngas	258	
QY	301	VKSCSHLHNKTMGMFNECGLANLINGIHHSGKFLATGIOMGIMTKNNSPVKIKTSVMKTR	360	
DB	259	vkschllhnktgmfnecglanlingihhsgkflatgiomgimtknnspvkiiktsvmktr	318	
QY	361	RMYNPFYK 368		
DB	319	rmynpfyk 326		

SEQUENCE	6	
ID	AAU14511	standard; Protein: 326 AA.
XX	AAU14511	
AC	AAU14511;	
XX		
DT	24-OCT-2001	(first entry)
XX		
DE	Human novel protein #382.	
XX		
KW	Human; novel protein; Antihaemic; osteopathic; antiinflammatory;	
KW	immunomodulatory; cytosolic; neuroprotective; vulnary; nocotropic;	
KW	anticonvulsant; antiallergic; cerebroprotective; antifungal; antiviral;	
KW	antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;	
KW	thrombolytic; immunogen; antibody; gene therapy; neurological disorder;	
KW	Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;	
KW	tissue regeneration; immune disorder.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200155437-A2.	
PD	02-AUG-2001.	
XX		
PF	25-JAN-2001; 2001WO-US02623.	
XX		
PR	25-JAN-2000; 2000US-0491404.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YF, Liu C, Drmanac RT;	
XX		
DR	WPI: 2001-451939/48.	
XX		
DR	N-PSDB: AAS22816.	
XX		
PT	Isolated polypeptides useful for treating anti-inflammatory diseases,	
XX	nervous system disorders, and for regenerating bone and cartilage -	
PS	Example 4; Page 848-849; 894pp: English.	
XX		
CC	The invention relates to polynucleotides encoding novel human	
CC	proteins or their active domains. The polypeptides, polynucleotides and	
CC	polypeptides raised against the polypeptides are used in a method of	
CC	treatment of a mammal and prevention of disorders caused by the aberrant	
CC	protein expression or activity. The polypeptides can be used as	
CC	molecular weight markers, food supplements, and in antibody production.	
CC	The polypeptides are used to identify compounds which bind to the	
CC	polypeptides. Polynucleotides of the invention are used as probes and	
CC	primers, for sequencing, for chromosome or gene mapping, in the	
CC	production of recombinant proteins, and in generating anti-sense DNA or	
CC	RNA and in gene therapy. Polypeptides of the invention can be used to	
CC	target drugs to a tumour. In assays to determine biological activity, to	
CC	raise antibodies/ elicit an immune response, to determine quantitative	
CC	protein levels, as tissue markers, and to isolate receptors or ligands.	
CC	Polypeptides of the invention may also be useful in treating platelet	
CC	disorders, stem cell disorders, regenerating bone, cartilage, tendon,	
CC	ligament and/or nerve tissue, wound healing, treating burns, promoting	
CC	the proliferation, differentiation and survival of stem cells, as a	
CC	contraceptive, treating osteoporosis and osteoarthritis, anaemia,	
CC	Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral	
CC	sclerosis, stroke, immune deficiencies resulting from bacterial, viral or	
CC	fungal infection or from autoimmunity, cancer, allergy, asthma,	
CC	graft-versus-host disease, eczema, haemophilia, thrombosis,	
CC	anti-inflammatory diseases, nervous system disorders, and infection.	
CC	The present sequence represents a protein of the invention.	
XX		
Sequence	326 AA;	

Query Match	81.2%;	Score 1625;	DB 22;	Length 326;
Best Local Similarity	83.28;	Pred. No. 2.7e-157;		
Matches 306; Conservative	0;	Mismatches 0;	Indels 62;	Gaps 1

```

OY      1 EVVQNCVHSHSTDSVNVIVEDGSSNAKDESKSNDTVCKEDCEESCDVKTITREKHFNC 60
        |||
        21 evvgncvshstsdssvnlvvedgsnakdesksndtvckedceescdvktitreekhnc 80
OY      61 RMLQNSIVSYTRSTKRLKLNMMDEQASLDYLSNQVNELMNVLLTTEVFRKQDPPFH 120
        |||
        Db 81 rnlqnsivsytrstckllrnmmdqgasldysnqvneilmnvllttevfrkqldppfh 140
OY      121 RPOVSHGLDCTDIKPTIGSVTKTPSGLYTIHPEGSSYPPEVWCDMDYRGGMVTIQRID 180
        |||
        Db 141 rpvshglctdtkptdigsvtktpsglytihpessyppevwcmndyrggwtvqkrtd 200
OY      181 GIIDFQRLMCDYLDGFGDLLGFEWLGKRIFYIVNQKNTSFMLVYALSEDDTLAVASYD 240
        |||
        Db 201 glidfgrlmcwyldgfgdll----- 220
OY      241 NFWLEDETRFFFKMHLGRYSGNAGDAFRGLKKEKEDNQNAFPSTSDVNDGCRPACLVNGQS 300
        |||
        Db 221 -----gdaftrglkckedngnampfstsdvndgcrpactlvngqs 258
OY      301 VKSCSHLNKGTGMWFNEGCLANLNGIHHSGLKLTATGIDMGTWTKNNSPVKIKSVSMKIR 360
        |||
        Db 259 vkscshlnhktgwfneegclanlngihhsghkllatgldgwtcknspvklksvsmkir 318
OY      361 RMVNPYFK 368
        |||
        Db 319 rmynpyfk 326

RESULT 7
ID      AAB82590
XX      AAB82590 standard; Protein; 326 AA.
XX
XX      AAB82590;
XX
DT      02-OCT-2001 (first entry)
XX
DE      Human prothrombinase-like polypeptide splice variant.
XX
KW      Prothrombinase-like polypeptide; human; haemostatic; cardiac;
KW      nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
KW      antiarteriosclerotic; anticancer; vulnerrary; osteoporosis;
KW      immunomodulatory; antineumatic; antitachytic; antinflammatory;
KW      thrombolytic; diagnosis; therapy.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Peptide
FT      Location/Qualifiers
FT      1..20
FT      /label= "Signal peptide"
FT      /note= "separately claimed in Claim 10"
FT      21..326
FT      /label= "Mature protein"
FT      /note= "separately claimed in Claim 10"
FT      181..217
FT      /note= "fibrinogen beta/gamma chain"
FT      262..293
FT      /note= "fibrinogen beta/gamma chain"
FT      82..321
FT      /note= "blood coagulation domain, separately
FT      claimed in Claim 10"
XX
XX      WO200153456-A2.
XX
XX      26-JUL-2001.
XX
XX      22-DEC-2000; 2000WO-US35061.
XX
XX      21-JAN-2000; 2000US-0488725.
XX      25-JAN-2000; 2000US-0491404.
XX      25-APR-2000; 2000US-0552317.
XX      17-JUN-2000; 2000US-0596196.
XX      31-AUG-2000; 2000US-0643313.

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XX      (HYSE-) HYSEQ INC.
PA      Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI      Arterburn MC, Tang YT, Liu C, Drmanac R;
DR      WPI: 2001-483140/52.
DR      N-PSDB: AAB26237.
XX
PT      Novel prothrombinase-like polypeptides and polynucleotides useful in
PT      diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS      Claim 10; Page 133; 140pp; English.
XX
XX

```

```

CC      The present sequence is that of a secreted, soluble splice variant
CC      of novel human secreted prothrombinase-like polypeptide (PLP, see
CC      also AAB82584). The splice variant has a predicted mol.wt. of
CC      37,000 (unglycosylated) and shows amino acid sequence similarity to
CC      human prothrombinase Fg12 protein. The sequence was predicted from
CC      a polynucleotide (see AAB26237) derived from a human ovary cDNA
CC      clone. PLP polynucleotides and polypeptides, including those
CC      comprising the mature protein, signal peptide or blood coagulation
CC      domain of the splice variant, can be used in the diagnosis,
CC      treatment and/or prevention of diseases associated with the
CC      dysregulation of coagulation pathways, such as haemophilia,
CC      myocardial infarction, glomerular disease, diabetes, fulminant viral
CC      hepatitis and atherosclerosis. They may also be beneficial in the
CC      treatment of viral infections and some forms of cancer. A claimed
CC      method of treating a subject in need of enhanced PLP activity or
CC      expression involves the administration of PLP, a PLP agonist or a
CC      polynucleotide encoding PLP. A claimed method of treating a subject
CC      having need to inhibit activity or expression of PLP involves the
CC      administration of a PLP antagonist, a polynucleotide that inhibits
CC      expression of a PLP polynucleotide, or a polypeptide that competes
CC      with the PLP for its ligand. The polypeptides can also be used to
CC      raise antibodies, as food supplements, and to screen for agonists
CC      and antagonists.
XX
SQ      Sequence 326 AA:

```

Query Match 81.2%; Score 1625; DB 22; Length 326;

Best Local Similarity 83.2%; Pred. No. 2,7e-157;

Matches 306; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

```

OY      1 EVVQNCVHSHSTDSVNVIVEDGSSNAKDESKSNDTVCKEDCEESCDVKTITREKHFNC 60
        |||
        Db 21 evvgncvshstsdssvnlvvedgsnakdesksndtvckedceescdvktitreekhnc 80
OY      61 RMLQNSIVSYTRSTKRLKLNMMDEQASLDYLSNQVNELMNVLLTTEVFRKQDPPFH 120
        |||
        Db 81 rnlqnsivsytrstckllrnmmdqgasldysnqvneilmnvllttevfrkqldppfh 140
OY      121 RPOVSHGLDCTDIKPTIGSVTKTPSGLYTIHPEGSSYPPEVWCDMDYRGGMVTIQRID 180
        |||
        Db 141 rpvshglctdtkptdigsvtktpsglytihpessyppevwcmndyrggwtvqkrtd 200
OY      181 GIIDFQRLMCDYLDGFGDLLGFEWLGKRIFYIVNQKNTSFMLVYALSEDDTLAVASYD 240
        |||
        Db 201 glidfgrlmcwyldgfgdll----- 220
OY      241 NFWLEDETRFFFKMHLGRYSGNAGDAFRGLKKEKEDNQNAFPSTSDVNDGCRPACLVNGQS 300
        |||
        Db 221 -----gdaftrglkckedngnampfstsdvndgcrpactlvngqs 258
OY      301 VKSCSHLNKGTGMWFNEGCLANLNGIHHSGLKLTATGIDMGTWTKNNSPVKIKSVSMKIR 360
        |||
        Db 259 vkscshlnhktgwfneegclanlngihhsghkllatgldgwtcknspvklksvsmkir 318
OY      361 RMVNPYFK 368
        |||
        Db 319 rmynpyfk 326

```

RESULT 8
 AAB82582 standard; Protein; 237 AA.
 ID AAB82582
 AC AAB82582;
 XX 02-OCT-2001 (first entry)
 XX Human prothrombinase-like polypeptide C-terminal region.
 DE
 XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cystostatic;
 KM antiarteriosclerotic; antileucic; vulnery; osteoporosis;
 KM immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
 KM thrombolytic; diagnosis; therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 236
 FT Misc-difference /note= "encoded by TTT"
 FT Misc-difference 237
 FT /note= "encoded by AAA"
 PN WO200153456-A2.
 XX 26-JUL-2001.
 PD
 XX 22-DEC-2000; 2000WO-US35061.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-JAN-2000; 2000US-0491404.
 PR 25-APR-2000; 2000US-0552317.
 PR 17-JUN-2000; 2000US-0596196.
 PR 31-AUG-2000; 2000US-0643313.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 XX Arterburn MC, Tang YT, Liu C, Drmanac R;
 PI WPI: 2001-483140/52.
 DR N-PSDB; AAB26233.
 DR
 XX Novel prothrombinase-like polypeptides and polynucleotides useful in
 PT diagnosing and treating e.g. myocardial infarction and diabetes -
 XX
 XX Example 2: Page 108; 140pp; English.
 PS
 XX The present sequence is that of the predicted protein translation
 CC product of a nucleic acid (see AAB26233) of the invention. It was
 CC deduced using software that selects a polypeptide based on a
 CC comparison of translated novel polynucleotides to known polypeptides.
 CC The sequence shows 38.462% identity to human fibrinogen-like
 CC protein, and corresponds to the C-terminal portion of a novel
 CC prothrombinase-like polypeptide (PLP, see AAB82583). PLPs can be
 CC in the diagnosis, treatment and/or prevention of diseases
 CC associated with the dysregulation of coagulation pathways, such as
 CC haemophilia, myocardial infarction, glomerular disease, diabetes,
 CC fulminant viral hepatitis and atherosclerosis. They may also be
 CC beneficial in the treatment of viral infections and some forms of
 CC cancer. A claimed method of treating a subject in need of enhanced
 CC PLP activity or expression involves the administration of PLP, a
 CC PLP agonist or a polynucleotide encoding PLP. A claimed method of
 CC treating a subject having need to inhibit activity or expression of
 CC PLP involves the administration of a PLP antagonist, a
 CC polynucleotide that inhibits expression of a PLP polynucleotide,
 CC or a polypeptide that competes with the PLP for its ligand.
 CC
 XX Sequence 237 AA;

Query Match 65.0%; Score 1299; DB 22; Length 237;
 Best Local Similarity 99.6%; Pred. No. 3.5e-124;
 Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 132 DIKPTIGSVTKTPSGGLYIHPEGSSYPEPEVWCDMDYRGGWTVIQKRIDGIIDFQRLMCD 191
 Db 1 dlkdltgsvtktpsgllyihpegssypepevwmcdmdyrggwtvqlkridgidfgrlwc 60
 OY 192 YLDGFGDLGFEFWLGKATFEYIVNOKNSFMLYVALESEDDTLVASYDNFLDERPEF 251
 Db 61 yldgfgdlgfefwlgkltfyivnqkntsmlyvalesedtlvasydnfldeetrff 120
 OY 252 KMHGGRYSGNAGDAFRGLKKEEDNONAMPSTSDVDNDCRACVNGSVKSCSHLHNT 311
 Db 121 kmhggrysgnagdafrglkkekdnqampfstsdvndgcrpactlvngsvkschlnhkt 180
 OY 312 GWMFNECGLANLNGIHHSGLLATGQWGTWTKNSFVKIKSVSMKIRMYNPY 366
 Db 181 gwmfnecglanlngihhsghllatgltqwtcknnsfvkiksvsmkirkmynp 235
 RESULT 9
 AAB82592
 ID AAB82592 standard; Protein; 240 AA.
 XX
 AC AAB82592;
 XX 02-OCT-2001 (first entry)
 DT
 XX Human prothrombinase-like polypeptide splice variant domain.
 DE
 XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cystostatic;
 KW antiarteriosclerotic; antileucic; vulnery; osteoporosis;
 KW immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
 KW thrombolytic; diagnosis; therapy; blood coagulation.
 XX
 XX Homo sapiens.
 OS
 XX WO200153456-A2.
 PN
 XX 26-JUL-2001.
 PD
 XX 22-DEC-2000; 2000WO-US35061.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-JAN-2000; 2000US-0491404.
 PR 25-APR-2000; 2000US-0552317.
 PR 17-JUN-2000; 2000US-0596196.
 PR 31-AUG-2000; 2000US-0643313.
 XX
 XX (HYSE-) HYSEQ INC.
 PA Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 XX Arterburn MC, Tang YT, Liu C, Drmanac R;
 PI WPI: 2001-483140/52.
 DR N-PSDB; AAB26237.
 DR
 XX Novel prothrombinase-like polypeptides and polynucleotides useful in
 PT diagnosing and treating e.g. myocardial infarction and diabetes -
 XX
 XX Claim 10: Page 134-135; 140pp; English.
 PS
 XX The present sequence is that of the blood coagulation domain of a
 CC secreted, soluble splice variant (see AAB82590) of novel human
 CC prothrombinase-like polypeptide (PLP). PLP polynucleotides and
 CC polypeptides, including those comprising the present domain of the
 CC PLP splice variant, can be used in the diagnosis, treatment and/or
 CC prevention of diseases associated with the dysregulation of
 CC coagulation pathways, such as haemophilia, myocardial infarction,
 CC glomerular disease, diabetes, fulminant viral hepatitis and
 CC atherosclerosis. They may also be beneficial in the treatment of

CC viral infections and some forms of cancer. A claimed method of
CC treating a subject in need of enhanced PLP activity or expression
CC involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.
CC
CC
CC
SQ Sequence 240 AA:

Query Match 63.2%; Score 1265; DB 22; Length 240;
Best Local Similarity 79.5%; Pred. No. 1.1e-120;
Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

QY 62 NQNSTVSTRSTKTLRMMDQASLDYLSNOVVELMNRVLLTTEVFRKQLDFPHR 121
DB 1 nqnsivstrstklrlmmdeqasldylsnqvnlmrvllltevfirkqlpfbphr 60
QY 122 PQQSHGLDCTDKRIGSVTKTPSGLYIHPGSSYFPEVMDMDYRGGMVYIQKRIG 181
DB 61 pvgshgldctdkrlgtvktcpsgilylhpogssyfpfemcdmdyrggwtvqkrldg 120
QY 182 IIDFORLWCMDYLDGFEDLLGEFVWLGIKRTFYLVNOKNTSFMVLALESDDTLAVASYDN 241
DB 121 iidfgrlwcodyldgfdll----- 139
QY 242 FWLEDETRFRKHLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVNDGCRPACLVNGOSV 301
DB 140 -----gdafgrlkkednqampstsdvdndgcrpactlvngsv 178
QY 302 KSCSHLHNKTMWFMNECGLANLNGIHMFSGKLLATGICQGTWTKNNSPVKIKSVSKIR 361
DB 179 kcschlhnktgwmfnecglanlngihfsgkllaiglgwtvcknpsvkiksvsmkrr 238
QY 362 MY 363
DB 239 my 240

RESULT 10
ABG22365
ID ABG22365 standard; Protein; 141 AA.
AC ABG22365;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22356.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS86552.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID NO 52724; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG3037 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 141 AA:

Query Match 31.7%; Score 634; DB 22; Length 141;
Best Local Similarity 64.3%; Pred. No. 1.5e-56;
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;

QY 158 PREVMCDMDYRGGMVYIQKRIGIIDFORLWCMDYLDGFEDLLGEFVWLGIKRTFYLVNOK 217
DB 9 plevmcdmdyrggwtvqkrldgiiidgrlwcodyldgfdll----- 51
QY 218 NTSFMLVLALESDDTLAVASYDNFWLEDETRFRKHLGRYSGNAGDAFRGLKKEEDNONA 277
DB 52 -----gdafgrlkkednqna 66
QY 278 MPFSTSDVNDGCRPACLVNGOSVKSCHLHNKTMWFMNECGLANLNGIHMFSGKLLATG 337
DB 67 mpfstsdvdndgcrpactlvngosvkschlhnktgwmfnecglanlngihfsgkllaig 126
QY 338 IOWGT 342
DB 127 lqwt 131

RESULT 11
ABG22361
ID ABG22361 standard; Protein; 138 AA.
XX
AC ABG22361;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22352.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR N-PSDB; AAS86548.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID NO 52720; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 138 AA;
Query Match 26.98; Score 538.5; DB 22; Length 138;
Best Local Similarity 62.38; Pred. No. 8.1e-47;
Matches 109; Conservative 0; Mismatches 1; Indels 65; Gaps 1;
QY 1 EVVQNCVHSTDSVNVIVEDGSNAKDESKSNDVCKEDESCDVKTITREKHFMC 60
Db 29 eavgnvhtstssvvnivedgsnakdesksndtvcckedescdvktitreekhmc 88
QY 61 RNLDNSTVSTRSTKTLRLNMDEQASLDYLSNQVNELMNRVLLTTEVFRKOLDPPPH 120
Db 89 rnlqnsivsytrstklkllrmmdqgalsdylnq----- 123
QY 121 RPVQSHLDCDIDKIDTIGSVTKTPSGLYIIHPBGSSYFPEVWCDMDYRGCGWTYI 175
Db 124 -----vmcdmdyrqgwtvl 138
RESULT 12
ID ABG22364
ID ABG22364 standard; Protein: 116 AA.
XX
AC ABG22364;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22355.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
PF
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR N-PSDB; AAS86551.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID NO 52723; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 116 AA;
Query Match 26.18; Score 521; DB 22; Length 116;
Best Local Similarity 93.18; Pred. No. 3.8e-45;
Matches 95; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 141 TKPSPGLYIIHPBGSSYFPEVWCDMDYRGCGWTYIQRIDGIFORLMCDYDGFGL 200
Db 13 tkpssglyihpbgssyfpewcmcdyrggwtvlvqkrlidgflrswsdyldgflv 72
QY 201 GEFMLGLKFIYIVNOKNTSFMLYVALESEDDTLAYASYDNF 242
Db 73 gefwlgllkflfyivnqkntftmlyvleseddpayalndf 114
RESULT 13
ID AAY26196
ID AAY26196 standard; Protein: 491 AA.
XX
AC AAY26196;
XX
DT 03-NOV-1999 (first entry)
XX
DE Human zapo3 protein.

XX		Human zapo3 protein; angiotensin-1; angiotensin-2, covalently linked;
KW		moleity; affinity tag; toxin; radionucleide; enzyme; fluorophore; multimer;
KV		coiled coil domain; carboxyl-terminal fibronogen-like domain; angiogenic;
KW		haemopoietic; mitogenic activity; angiogenesis; inhibitor;
KW		endocrine-vascular cell association; revascularisation; DNA probe;
KX		neuronal degeneration; anti-zapo3 antibody.
XX		
OS	Homo sapiens.	
XH	Key	Location/Qualifiers
FT	Peptide	1..21
FT	Peptide	/label= Secretory-Signal-Sequence
FT	Peptide	43..48
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	93..98
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	120..125
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	421..426
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Peptide	422..427
FT	Peptide	/label= Immunogen
FT	Peptide	/note= "For production of antibodies"
FT	Domain	279..490
FT	Domain	/label= Fibrinogen-like-domain
FT	Domain	/note= "Homologous to residues 631-864 of human fibrinogen alpha chain "
FT	Domain	63..253
FT	Domain	/label= Amino-terminal-coiled_coil_domain
FT	Misc-difference	280
FT	Misc-difference	/note= "Conserved cysteine residue"
FT	Misc-difference	309
FT	Misc-difference	/note= "Conserved cysteine residue"
FT	Misc-difference	432
FT	Misc-difference	/note= "Conserved cysteine residue"
FT	Misc-difference	445
FT	Misc-difference	/note= "Conserved cysteine residue"
XX		
PN	WO9940193-A1.	
XX		
PD	12-AUG-1999.	
XX		
PE	03-FEB-1999;	99WO-US02303.
PR	04-FEB-1998;	98US-0018258.
XX		
PA	(ZYMO) ZYMOGENETICS INC.	
XX		
PI	Holloway JL, Shoemaker KE;	
XX		
DR	WP1; 1999-508503/42.	
XX	N-PSDB; AAX80866.	
PT	Human angiotensin homologue, ZAPO3 useful for study and regulation	
PT	of angiogenesis	
XX		
PS	Claim 1; Page 65-67; 78pp; English.	
XX		
CC	The present sequence is a human zapo3 protein. Zap3 protein exhibits	
CC	significant amino acid sequence homology to angiotensin-1 and 2. It is	
CC	covalently linked to a moiety chosen from affinity tags, toxins,	
CC	radionucleides, enzymes and fluorophores. The protein is assembled as a	
CC	multimer and is characterized by an amino-terminal coiled coil domain and	
CC	a carboxyl-terminal fibronogen-like domain. Zap3 has angiogenic,	
CC	haematopoietic and mitogenic activity. It is useful in the study and	
CC	regulation of angiogenesis, and for developing inhibitors of	
CC	angiogenesis. It is possibly involved in modulation of endocrine-vascular	
CC	cell association and may be used therapeutically to stimulate the	

CC	revascularisation of tissue, to promote angiogenesis and prevent neuronal
CC	degeneration. DNA probes and anti-zap03 antibodies can be used to detect
CC	sides of angiogenesis.
xx	
SO	Sequence 491 AA:
Query Match	21.2%; Score 425; DB 20; Length 491;
Best Local Similarity	26.9%; Pred. No. 2.2e-34;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14	
OY	24 SNADDEKSDNTYCKEKECESCVKRTKIRE-EKHMCMNLONSIVSTRSKILLRMM 82
Db	68 tkqgdaastikxmiIrmIdenlkvdlsrqkrelvdqlvldvdgnlvevklfrkesrnm 127
OY	83 DE-QQASLDYV-----SNQNELMNRVLTLTTE----- 109
Db	128 srvtqqlymqllheItrkdnslsqtlenklntvtemlkmalttryrelvxyastIdvln 187
OY	110 -----VERKO--LDP-----FPRHPVOSHGL----- 128
Db	188 ngsvmiellleeqcltrfsrqtthvsppIvqvvpqhIpnsgytlpqllganeIqrqpyr 247
OY	129 DCTDIKDTIGSVKTP-----SGLYIIHPGSSYPREV 161
Db	248 dImpprdlaatsrpkIppvtflneagpfkdcgqakeahsvsgIylmkprensngpmql 307
OY	162 MCDMDYRGGGGTVAQKRIIDGIDFORLMCDYLDGFEDLLGEFMILGKRTFYVNOKNTSF 221
Db	308 wcemsIspgwtvktqktsgsvnfInwenyakkqfgnIdgeywlIdenIymIsngdn--y 365
OY	222 MLYVALESEDDTLAASYNFMLEDETRFEKMHGKRYSGMAGDAERGLKKEEDNQAMPFS 281
Db	366 kllleledwsdkvyaesfrIepesefyrlrlgfygngagdsnmw-----hngkqft 419
OY	282 TSDVDNOCRAPACLVNQSKSCSHLHNTGMMFNFCGLANLNGIHHSKLLA---TGI 338
Db	420 fIdrckd-----mYagncahfh-KygwWynaCaShnIngWYrgbhyrskhgqI 468
OY	339 QMGTWTKNNSPVRKISVSKMR 360
Db	469 fwaey--rfgsystIraVgmmlk 488
RESULT 14	
AAV05397	
ID	AAV05397 standard; Protein; 491 AA.
XX	
AC	AAV05397;
XX	
DT	01-JUL-1999 (first entry)
XX	
DE	Human TIE ligand NL5 protein sequence.
XX	
KW	Human TIE ligand; NL1; NL4; NL5; NL8; Ig homology domain; angiogenesis;
KW	EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
KW	early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
KW	endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
KW	vasculogenesis; detection; diagnosis; therapy.
XX	
OS	Homo sapiens.
XX	
PN	W09915653-A2.
XX	
PD	01-APR-1999.
XX	
PF	14-SEP-1998; 98WO-US19093.
XX	
PR	29-OCT-1997; 97US-0960507.
PR	19-SEP-1997; 97US-0933821.
XX	
PA	(GETH) GENENTECH INC.
XX	

PI Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;
 PI Hillan K, Roy M, Schwall R, Tumas D;
 XX WPI; 1999-263480/22.
 DR N-PSDB; AAX36342.
 XX
 PT New isolated TIE ligand homologs for, e.g. developing products for
 PT treatment of tumors
 PS
 XX Claim 8; Fig 5; 132pp; English.
 XX
 CC This sequence is the human tyrosine kinase containing Ig and EGF
 CC homology domains (TIE) ligand of the invention, designated NL5.
 CC The TIE receptors are receptor tyrosine kinases which are expressed in
 CC vascular endothelial cells and early hemopoietic cells. The TIE
 CC receptors are believed to be actively involved in angiogenesis, and may
 CC play a role in hemopoiesis as well. The TIE ligand homologs can promote
 CC the survival and/or growth and/or differentiation of TIE receptor
 CC expressing cells. They can be used for promoting neovascularisation in
 CC wound healing and for promoting angiogenic processes, such as for
 CC inducing collateral vascularisation in an ischemic heart or limb, or for
 CC promoting bone development and/or maturation and/or growth in a patient
 CC or muscle growth and development. The TIE ligand homologs and antibodies
 CC can inhibit the growth of endothelial cells and induce apoptosis of
 CC cells, particularly tumour cells. They can inhibit vasculogenesis.
 CC particularly the vascularisation of tumour cells. The antibodies can also
 CC inhibit vascularisation of a cell in which a gene encoding an NL1, NL5,
 CC N18 or N14 polypeptide is amplified. The products can also be used for
 CC detection, diagnosis, drug screening and production of transgenic
 CC animals.
 CC
 XX
 XX Sequence 491 AA:
 SQ

Query Match 21.2%; Score 425; DB 20; Length 491;
 Best Local Similarity 26.9%; Pred. No. 2.2e-34;
 Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 24 SNADESKNDYVCKEDCECDYKTKTR-EKHFMCRNQNSIVSTRSKLLRRMM 82
 DB 68 tkqdaatlkdmltrmdlenkdvlsrqreldvqlvvdvgnlvekvllkrstrmn 127
 QY 83 DE-QQASLDLV-----SNOVLEIMNRYLLTTE----- 109
 DB 128 srvgqlmqllheltkrdnslsleqleknklnvtemlkatyrelvyaaltldvn 187
 QY 110 -----VFRKQ---LDP-----PFRPVQSHGL----- 128
 DB 188 nqsvmlclleeqclrfstqthvsprlvqvpqhlpnsqyltpglglsneigrdpypr 247
 QY 129 DCTIKRTIGSVTKP-----SGLYIIEGSSYPREV 161
 DB 248 dlmpplalatspfskfpkfpvflneqpfkdcgqakeaghsvsqlymklpensnqpmql 307
 QY 162 MCDMDYRGSGWTVQKRGDIIDFQRLMCDYLDGFDLLGEFGLKKEIFIVOKNTSF 221
 DB 308 wceasldpgyvtvlgkrtidsgvnmfrfwmkkgfmgdgywlgleniylnsqdn-y 365
 QY 222 MLVVALESEDDTLAVASYDNFMLEDETRFFKMLGRYSGNAGDAFRLKEDNONAMPFS 281
 DB 366 klileedwskkvyaeysfrlepesefyrlrlgtygnagdsmmw-----hngkft 419
 QY 282 TSDVDNOCGRACLVNQSOSVSCSHLNKTKGWMFNEGGLANLNIHFSGLLA---TGI 338
 DB 420 clldcdk-----myagncahfh-kqgwvwnacahsnlgnvvyrgyhrskhdgyl 468
 QY 339 QMGWTKNNSPVKIKTSVMKIR 360
 DB 469 fwaey--rgsgyslrvavmmik 488

ID AAB24393 standard; Protein: 491 AA.
 XX AAB24393;
 AC
 XX 07-NOV-2000 (first entry)
 DT
 XX
 DE Human PRO188 protein sequence SEQ ID NO:26.
 XX
 KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
 KW cytoskeletal; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 PN WO200032221-A2.
 PD 08-JUN-2000.
 XX
 PF 30-NOV-1999; 99WO-US28313.
 XX
 PR 01-DEC-1998; 98WO-US25108.
 PR 16-DEC-1998; 98US-0112850.
 PR 12-JAN-1999; 99US-0115554.
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker RP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
 PI Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
 PI Watanabe CK, Williams PM, Wood WT;
 XX
 XX WPI; 2000-412154/35.
 DR N-PSDB; AAA77529.
 XX
 PT Nucleic acids encoding PRO polypeptides useful for preventing,
 PT diagnosing and treating disorders a cardiovascular, endothelial or
 PT angiogenic disorders in mammals -
 PS
 PS Claim 72; Fig 12; 315pp; English.
 XX
 CC The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating disorders in mammals by
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PRO expression such as cardiovascular, endothelial or
 CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
 CC cardiac hypertrophy). For example, the nucleic acids (NAs) and vectors
 CC containing them and the PRO polypeptide may be used to treat disorders
 CC associated with decreased PRO expression. AAA77510 to AAA77721 and
 CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
 CC the exemplification of the present invention.
 CC
 XX Sequence 491 AA;
 SQ

RESULT 15
 AAB24393

[illegible]

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FT      /note= "fibrinogen beta/gamma chain"
FT      /note= "separately claimed in Claim 10"
PN      WO200153456-A2.
XX      26-JUL-2001.
PD      22-DEC-2000; 2000WO-US35061.
PF      21-JAN-2000; 2000US-0488725.
XX      25-JAN-2000; 2000US-0491404.
PR      25-APR-2000; 2000US-0552317.
PR      17-JUN-2000; 2000US-0596196.
PR      31-AUG-2000; 2000US-0643313.
XX      (HYSE-) HYSEQ INC.
XX      PA
XX      PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI      Arterburn MC, Tang YT, Liu C, Drmanac R;
XX      DR WPI: 2001-483140/52.
XX      DR N-PSDB; AAH26235, AAH26236.
XX      PT Novel prothrombinase-like polypeptides and polynucleotides useful in
XX      PT diagnosing and treating e.g. myocardial infarction and diabetes -
XX      PS Claim 10; Page 126-127; 140pp; English.
XX      XX
XX      CC The present sequence is that of a novel human secreted
XX      CC prothrombinase-like polypeptide (PLP). The polypeptide has a
XX      CC predicted mol.wt. of 43,000 (unglycosylated) and shows amino acid
XX      CC sequence similarity to human prothrombinase Fg12 protein. The
XX      CC sequence was predicted from polynucleotides (see AAH26235-36)
XX      CC derived from a human ovary cDNA clone. PLP polynucleotides and
XX      CC polypeptides, including the mature protein, polypeptides including
XX      CC PLP fibrinogen chains, and a soluble splice variant (see AAH82590),
XX      CC can be used in the diagnosis, treatment and/or prevention of diseases
XX      CC associated with the dysregulation of coagulation pathways, such as
XX      CC haemophilia, myocardial infarction, glomerular disease, diabetes,
XX      CC fulminant viral hepatitis and atherosclerosis. They may also be
XX      CC beneficial in the treatment of viral infections and some forms of
XX      CC cancer. A claimed method of treating a subject in need of enhanced
XX      CC PLP activity or expression involves the administration of PLP, a
XX      CC PLP agonist or a polynucleotide encoding PLP. A claimed method of
XX      CC treating a subject having need to inhibit activity or expression of
XX      CC PLP involves the administration of a PLP antagonist, a
XX      CC polynucleotide that inhibits expression of a PLP polynucleotide,
XX      CC or a polypeptide that competes with the PLP for its ligand. The
XX      CC polypeptides can also be used to raise antibodies, as food
XX      CC supplements, and to screen for agonists and antagonists.
XX      CC
SQ      Sequence 388 AA;

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QY      241 FMLYVALESEDDTLAYASYADYNFMLEDETRFFKMHILGRYSGNAGDAFRGLKEDQNPMPF 300
DB      241 fmlvaleseeddtlayasydnfmlēdetrffkmhilygrysnagdafrglkēdqnmpf 300
QY      301 STSDVNDGCRPACLYNGOSVSKSHLHKTKGWFRECGLANLNGIHFSGLATGIOW 360
DB      301 stsdvndgcrpactlyngosvskshlnkcgwfnecglanlngihfsgkllatgiqw 360
QY      361 GMTKKNNSPVKIKRSVSMKIRRMYNPYEK 388
DB      361 gmtkknnsppvklksvsmkltmrynpyk 388

RESULT 2
AAV72622
ID      AAV72622 standard; Protein: 388 AA.
XX      AC AAV72622;
XX      DT 02-MAY-2001 (first entry)
XX      DE Human angiotensin protein, CG144.
XX      KW Human; angiotensin; angiotensin; gene therapy; CG144;
KW      vascular stability; neovascularisation; nutritional supplement; therapy;
KW      myocardial infarction; proliferative retinopathy; atherosclerosis;
KW      coronary heart disease; arterial ischaemia; bone disorder; cancer;
KW      abnormal vascular growth; anaemia; chronic inflammation; immune disorder;
KW      haematopoiesis related disorder; coagulation disorder; leukaemia;
KW      cytostatic; vasotropic; food supplement; nervous system disorder;
XX      OS Homo sapiens.
XX      FH Key
XX      FT Peptide
XX      FT 1..22
XX      FT /label= Signal_peptide
XX      FT Protein
XX      FT 23..388
XX      FT /note= "Mature angiotensin protein, CG144"
XX      FT Domain
XX      FT 193..230
XX      FT /note= "Fibrinogen domain"
XX      FT Domain
XX      FT 234..247
XX      FT /note= "Fibrinogen domain"
XX      FT Domain
XX      FT 283..301
XX      FT /note= "Fibrinogen domain"
XX      FT Domain
XX      FT 307..321
XX      FT /note= "Fibrinogen domain"
XX      FT Domain
XX      FT 337..366
XX      FT /note= "Fibrinogen domain"
XX      PN WO200105825-A2.
XX      PD 25-JAN-2001.
XX      PF 17-JUL-2000; 2000WO-US19429.
XX      PR 16-JUL-1999; 99US-0354881.
XX      PA (HYSE-) HYSEQ INC.
XX      PI Ballinger DG, Montgomery JR;
XX      DR WPI: 2001-091966/10.
XX      DR N-PSDB; AAD02607.
XX      PT Human angiotensin proteins and DNA encoding sequences useful for
XX      PT preventing, treating or ameliorating a medical condition in a mammalian
XX      PT subject e.g. arthritis and cancer -
XX      PS Claim 10; Page 111-112; 132pp; English.
XX      CC The present sequence is human angiotensin protein, CG144.

```


OY 201 GIIDFQRLWCYLDLGGDLGFEFWLGLKKIPIYVNOKNTPSEMLVYALSEEDDTLAYASVD 260
CC |||||||
CC 181 glidfglrwcdyldgfgdligefwlgkklfylnqknsfmlyalaseeddtlayasyd 240
DB |||||||
OY 261 NWLDEPFEEFMHIGRYSGNAGDAFRGLKKEDNONAMPEFSVDNDGCRPACLVNGOS 320
CC |||||||
DB 241 ntlwledetrffmhlgrysgnagdrlgklednqampfscsdvdndgcrpactlvngqs 300
CC |||||||
OY 321 VKSCHLHNKKTGMWFNECGLANLNGIHNFSGLATGIGMGTWTKNNSPVKIKISVSMKIR 380
CC |||||||
DB 301 vkschlnhktgwmfnecglanlngihfsgklatgltgwgctcknspvklksvsmkir 360
CC |||||||
OY 381 RMYNPFYK 388
CC |||||||
DB 361 rmynpfyk 368
CC |||||||

RESULT 4
AAU14275
ID AAU14275 standard; Protein: 326 AA.
XX
AC AAU14275;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #146.
XX
XX Human; novel protein; Antianaemic; osteopathic; antinflammatory;
KW immunomodulatory; cytosarctic; neuroprotective; vulnerability; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW chromolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
XX Homo sapiens.
OS
XX WO200155437-A2.
PN
XX 02-AUG-2001.
PD
XX 25-JAN-2001; 2001WO-US02623.
PE
XX 25-JAN-2000; 2000US-0491404.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Drmanac RT;
PI
XX WPI: 2001-451939/48.
DR
XX N-PSDB: AAS22580.
XX
PT Isolated polypeptides useful for treating anti-inflammatory diseases,
PT nervous system disorders, and for regenerating bone and cartilage -
XX
PS Example 4; Page 605; 894pp; English.
PS
XX The invention relates to polynucleotides encoding novel human
CC proteins or their active domains. The polypeptides, polynucleotides and
CC antibodies raised against the polypeptides are used in a method of
CC treatment of a mammal and prevention of disorders caused by the aberrant
CC protein expression or activity. The polypeptides can be used as
CC molecular weight markers, food supplements, and in antibody production.
CC The polypeptides are used to identify compounds which bind to the
CC polypeptides. Polynucleotides of the invention are used as probes and
CC primers, for sequencing, for chromosome or gene mapping, in the
CC production of recombinant proteins, and in generating anti-sense DNA or
CC RNA and in gene therapy. Polypeptides of the invention can be used to
CC target drugs to a tumour, in assays to determine biological activity, to
CC raise antibodies/elicits an immune response, to determine quantitative
CC protein levels, as tissue markers, and to isolate receptors or ligands.
CC Polypeptides of the invention may also be useful in treating platelet

CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
CC ligament and/or nerve tissue, wound healing, treating burns, promoting
CC the proliferation, differentiation and survival of stem cells, as a
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
CC fungal infection or from autoimmunity, cancer, allergy, asthma,
CC graft-versus-host disease, eczema, haemophilia, thrombosis,
CC anti-inflammatory diseases, nervous system disorders, and infection.
CC The present sequence represents a protein of the invention.
XX
SQ Sequence 326 AA.

Query Match 82.2%; Score 1729; DB 22; Length 326;
Best Local Similarity 84.0%; Pred. No. 7e-167;
Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

OY 1 MNSPQASLLFLNVCIFGTGGEVYQGCNHNSTDSVYVIVEDGSNAKDESKNDYCKED 60
DB 1 mnspsqasllflnvcifgtggevvgncvhnstsdsvvnlvedgsnakdesksndtcked 60
OY 61 CEESCDVKTITPEEKHFMCRLNNSIVSTRSTKLLRNMDQOASLDYLSNOVNEIM 120
DB 61 ceescdvkktitpeekhfmcrlnngnsivstrstkllrnmdeqasldysngvneim 120
OY 121 NRYLLTTEVFRKQDPPFRPVQSHGLDCTDKITGIVTTPSGLYIHNEGSSYPE 180
DB 121 nryllttevfrkqldppfrpvsngldctdkitgvtvtpsglyllhpegsypfe 180
OY 181 VNCMDMYRGGWTVIDKRIIDGIDFQRLWCYLDLGGDLGFEFWLGLKKIPIYVNOKN 240
DB 181 vncmdmyrggwvltvldkridgidfgrlwcylldgfgdlgfefwlgkklfpiyvnokn 220
OY 241 FMLVYALSEEDDTLAYASYDNFWLEDETRFFKMLHGRYSGNAGDAFRGLKKEDNONAMP 300
DB 221 -----gdaftrglklednqampf 238
OY 301 STSDVDNDGCRPACLVNGOSVKSCHLHNKTMWFNECGLANLNGIHNFSGLATGIG 360
DB 239 stsdvndgcrpactlvngqsvkschlnhktgwmfnecglanlngihfsgklatgigw 298
OY 361 GTWTKNNSPVKIKISVSMKIRMYNPFYK 388
DB 299 gwtcknspvklksvsmkirrmynpfyk 326

RESULT 5
AAU14511
ID AAU14511 standard; Protein: 326 AA.
XX
AC AAU14511;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human novel protein #382.
XX
XX Human; novel protein; Antianaemic; osteopathic; antinflammatory;
KW immunomodulatory; cytosarctic; neuroprotective; vulnerability; nootropic;
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
KW antibacterial; antiallergic; dermatological; haemostatic; antiaesthetic;
KW chromolytic; immunogen; antibody; gene therapy; neurological disorder;
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
KW tissue regeneration; immune disorder.
XX
XX Homo sapiens.
OS
XX WO200155437-A2.
PN
XX 02-AUG-2001.
PD
XX 25-JAN-2001; 2001WO-US02623.
PE
XX

PR 25-JAN-2000; 2000US-0491404.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI: 2001-451939/48.
 DR N-PSDB: AAS22816.
 XX Isolated polypeptides useful for treating anti-inflammatory diseases,
 PT nervous system disorders, and for regenerating bone and cartilage -
 XX
 PS Example 4; Page 848-849; 894pp; English.
 XX
 CC The invention relates to polynucleotides encoding novel human
 CC proteins or their active domains. The polypeptides, polynucleotides and
 CC antibodies raised against the polypeptides are used in a method of
 CC treatment of a mammal and prevention of disorders caused by the aberrant
 CC protein expression or activity. The polypeptides can be used as
 CC molecular weight markers, food supplements, and in antibody production.
 CC The polypeptides are used to identify compounds which bind to the
 CC polypeptides. Polynucleotides of the invention are used as probes and
 CC primers, for sequencing, for chromosome or gene mapping, in the
 CC production of recombinant proteins, and in generating anti-sense DNA or
 CC RNA and in gene therapy. Polypeptides of the invention can be used to
 CC target drugs to a tumour, in assays to determine biological activity, to
 CC raise antibodies/elicit an immune response, to determine quantitative
 CC protein levels, as tissue markers, and to isolate receptors or ligands.
 CC Polypeptides of the invention may also be useful in treating platelet
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting
 CC the proliferation, differentiation and survival of stem cells, as a
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,
 CC anti-inflammatory diseases, nervous system disorders, and infection.
 CC The present sequence represents a protein of the invention.
 CC
 XX
 XX
 SQ Sequence 326 AA:
 Query Match 82.2%; Score 1729; DB 22; Length 326;
 Best Local Similarity 84.0%; Pred. No. 7e-167;
 Matches 326; Conservative 0; Mismatches 0; Indels 62; Gaps 1;
 QY 1 MMSPSQASLFLNVCIFIGEVGQNCVHNSSTSSVNIIVEDGSNAKDESKSNDTCKED 60
 DB 1 mmspsqasllflnvcifigevgncvhsstssvniivedgsnakdesksndtcked 60
 QY 61 CEESCDVWTKTRREKHMCRNLNLSYSTRSKTKLLRNAMDQASLDYLSNOVNL 120
 DB 61 ceescdvwtkttrrekhmcrnl nlsystrsktkllrnmddqasldylsnovnelm 120
 QY 121 NRVLITTEVERKQLDPPHPRVOSHGLDCTDKTIGSVTKTPSGLYTIIPESGSYPE 180
 DB 121 nrvlittevtrkqlpphprvoshgldctdkdtisvktkpsglytiipegsypfe 180
 QY 181 VMCDMDYRGGMWTVIQKRIDGIDFQRLMCDYLDGFGDLGEFWLGLKRIEYVQNKTS 240
 DB 181 vmcdmdyrggmwvtyiqkridgidfqrllmcdyldgfgdlgefmlglkrieyvqnkts 240
 QY 241 FMLYVALESEDDTLAYASYDNFWLEDFTRFRKMLGRISGNAGDAFRGLKKEDNONAMP 300
 DB 241 fmlvaleseddtlayasydnfwledftrfrkmlgrisgnagdafrglkkednonamp 300
 QY 301 STSDVDNCGCPACLVNCGSVKCSHLNKTGMWFECCGLANLNGIHHSGLKLTATGIOW 360
 DB 301 stsdvndngcpcpactlvnngsvkcschlnktgmwfeccglanlngihhsghlktatgiow 360
 QY 361 GTWTKNNSPVKIKSVSMKIRRMYNPFYK 388
 DB 361 gtwtknnsppvki ksvsmkrrmynpfyk 388

DB 299 gtwtknnsppvki ksvsmkrrmynpfyk 326
 RESULT 6
 ID AAB82590 standard; Protein; 326 AA.
 AC AAB82590;
 XX 02-OCT-2001 (first entry)
 XX
 XX Human prothrombinase-like polypeptide splice variant.
 DE
 XX Prothrombinase-like polypeptide; human; haemostatic; cardiac;
 KW nephrotropic; antidiabetic; hepatotropic; antiviral; cytostatic;
 KW antidiabetic; antitumor; anticancer; vulnary; osteoporosis;
 KW immunomodulatory; antineoplastic; antirheumatic; antiinflammatory;
 XX thrombolytic; diagnosis; therapy.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /label= Signal_peptide
 FT /note= "separately claimed in Claim 10"
 FT Protein 21..326
 FT /label= Mature_protein
 FT /note= "separately claimed in Claim 10"
 FT Domain 181..217
 FT /note= "fibrinogen beta/gamma chain"
 FT Domain 262..292
 FT /note= "fibrinogen beta/gamma chain"
 FT Domain 82..321
 FT /note= "blood coagulation domain, separately
 FT claimed in Claim 10"
 XX
 PD WO200153456-A2.
 XX 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-US35061.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-JAN-2000; 2000US-0491404.
 PR 25-APR-2000; 2000US-0552317.
 PR 17-JUN-2000; 2000US-0596196.
 PR 31-AUG-2000; 2000US-0643313.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
 PI Arterburn MC, Tang YT, Liu C, Drmanac R;
 DR WPI: 2001-483140/52.
 DR N-PSDB: AAB26237.
 XX
 PT Novel prothrombinase-like polypeptides and polynucleotides useful in
 PT diagnosing and treating e.g. myocardial infarction and diabetes -
 XX
 PS Claim 10; Page 133; 140pp; English.
 XX
 CC The present sequence is that of a secreted, soluble splice variant
 CC of novel human secreted prothrombinase-like polypeptide (PLP, see
 CC also AAB82584). The splice variant has a predicted mol. wt. of
 CC 37,000 (unglycosylated) and shows amino acid sequence similarity to
 CC human prothrombinase Fg12 protein. The sequence was predicted from
 CC a polynucleotide (see AAB26237) derived from a human ovary cDNA
 CC clone. PLP polynucleotides and polypeptides, including those
 CC comprising the mature protein, signal peptide or blood coagulation
 CC domain of the splice variant, can be used in the diagnosis,
 CC treatment and/or prevention of diseases associated with the
 CC dysregulation of coagulation pathways, such as haemophilia,
 CC myocardial infarction, glomerular disease, diabetes, fulminant viral


```

RESULT      8
AAB82582
ID   AAB82582 standard; Protein; 237 AA.
XX
AC   AAB82582;
XX
DT   02-OCT-2001 (first entry)
XX
DE   Human prothrombinase-like polypeptide C-terminal region.
XX
KW   Prothrombinase-like polypeptide; human; haemostatic; cardiant;
KW   nephrotropic; antidiabetic; hepatotropic; antiviral; cyostatic;
KW   antiarteriosclerotic; anticulcer; vulnery; osteoporosis;
KW   immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
KW   thrombolytic; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
FH   Key
FT   Misc-difference 236
FT   Misc-difference 237 /note="encoded by TTT"
FT   Misc-difference 237 /note="encoded by AAA"
XX
PN   WO200153456-A2.
XX
PD   26-JUL-2001.
XX
PE   22-DEC-2000; 2000WO-US35061.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-JAN-2000; 2000US-0491404.
PR   25-APR-2000; 2000US-0552317.
PR   17-JUN-2000; 2000US-0596196.
PR   31-AUG-2000; 2000US-0643313.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI   Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
DR   N-PSDB; AAB26233.
XX
PT   Novel prothrombinase-like polypeptides and polynucleotides useful in
PT   diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS   Example 2; Page 108; 140pp; English.
XX
CC   The present sequence is that of the predicted protein translation
CC   product of a nucleic acid (see AAB26233) of the invention. It was
CC   deduced using software that selects a polypeptide based on a
CC   comparison of translated novel polynucleotides to known polypeptides.
CC   The sequence shows 38.462% identity to human fibrinogen-like
CC   protein, and corresponds to the C-terminal portion of a novel
CC   prothrombinase-like polypeptide (PLP, see AAB82583). PLPs can be
CC   in the diagnosis, treatment and/or prevention of diseases
CC   associated with the dysregulation of coagulation pathways, such as
CC   haemophilia, myocardial infarction, glomerular disease, diabetes,
CC   fulminant viral hepatitis and atherosclerosis. They may also be
CC   beneficial in the treatment of viral infections and some forms of
CC   cancer. A claimed method of treating a subject in need of enhanced
CC   PLP activity or expression involves the administration of PLP, a
CC   PLP agonist or a polynucleotide encoding PLP. A claimed method of
CC   treating a subject having need to inhibit activity or expression of
CC   PLP involves the administration of a PLP antagonist, a
CC   polynucleotide that inhibits expression of a PLP polynucleotide,
CC   or a polypeptide that competes with the PLP for its ligand.
XX
SQ   Sequence      237 AA;

```

```

Query Match      61.7%; Score 1299; DB 22; Length 237;
Best Local Similarity 99.6%; Pred. No. 2,1e-123;
Matches 234; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 152 DIKDTIGSVTKTPSGLYIIMPEGSSYPEVYVCMDDYRGCGWTVIQKRIDGIIDFQRLMCD 211
DB 1 dlkdltigsvktktpsglyilimpegssypfevmcndmdyrgcgwtvqkrldgidlfdqrlwcd 60
QY 212 YLDGFGDLGFEFWGLKRIPIYVQKNTSFMLYVALESDDTLVASYDNFWLEDETRFF 271
DB 61 yldgfgdlgfefwglkripiyvnqkntsfmllyalesddtlvaysydnfwledeff 120
QY 272 KMHLGRSGNAGDPEFRGLKREDDNONAMPFSVDVNDGCRACVWNGSVKCSHLNKT 331
DB 121 kmhlgrysgnaagdafrglkrednqampfscsdvndgcrpactlvnqsvkscshlnkt 180
QY 332 GWMFNECGLANLNGIHHSKRLATGIQMGTWTRNNSPVKIKSVSMKIRRMYPY 386
DB 181 gwmfnecglanlngihhtsgkllatgiqmgwtwtrnnsrvkiksvsmkirmrnpny 235

RESULT      9
AAB82592
ID   AAB82592 standard; Protein; 240 AA.
XX
AC   AAB82592;
XX
DT   02-OCT-2001 (first entry)
XX
DE   Human prothrombinase-like polypeptide splice variant domain.
XX
KW   Prothrombinase-like polypeptide; human; haemostatic; cardiant;
KW   nephrotropic; antidiabetic; hepatotropic; antiviral; cyostatic;
KW   antiarteriosclerotic; anticulcer; vulnery; osteoporosis;
KW   immunomodulatory; antirheumatic; antiarthritic; antiinflammatory;
KW   thrombolytic; diagnosis; therapy; blood coagulation.
XX
OS   Homo sapiens.
XX
PI   WO200153456-A2.
XX
PD   26-JUL-2001.
XX
PE   22-DEC-2000; 2000WO-US35061.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-JAN-2000; 2000US-0491404.
PR   25-APR-2000; 2000US-0552317.
PR   17-JUN-2000; 2000US-0596196.
PR   31-AUG-2000; 2000US-0643313.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Haley DA, Boyle BJ, Suk-Yue Ho A, Zhou P, Mize NK, Kuo C;
PI   Arterburn MC, Tang YT, Liu C, Drmanac R;
XX
DR   N-PSDB; AAB26237.
XX
PT   Novel prothrombinase-like polypeptides and polynucleotides useful in
PT   diagnosing and treating e.g. myocardial infarction and diabetes -
XX
PS   Claim 10; Page 134-135; 140pp; English.
XX
CC   The present sequence is that of the blood coagulation domain of a
CC   secreted, soluble splice variant (see AAB82590) of novel human
CC   prothrombinase-like polypeptide (PLP). PLP polynucleotides and
CC   polypeptides, including those comprising the present domain of the
CC   PLP splice variant, can be used in the diagnosis, treatment and/or
CC   prevention of diseases associated with the dysregulation of
CC   coagulation pathways, such as haemophilia, myocardial infarction,
CC   glomerular disease, diabetes, fulminant viral hepatitis and
CC   atherosclerosis. They may also be beneficial in the treatment of

```

CC viral infections and some forms of cancer. A claimed method of
CC treating a subject in need of enhanced PLP activity or expression
CC involves the administration of PLP, a PLP agonist or a
CC polynucleotide encoding PLP. A claimed method of treating a subject
CC having need to inhibit activity or expression of PLP involves the
CC administration of a PLP antagonist, a polynucleotide that inhibits
CC expression of a PLP polynucleotide, or a polypeptide that competes
CC with the PLP for its ligand. The polypeptides can also be used to
CC raise antibodies, as food supplements, and to screen for agonists
CC and antagonists.
CC
XX
SQ Sequence 240 AA:

Query Match 60.1%; Score 1265; DB 22; Length 240;
Best Local Similarity 79.5%; Pred. No. 6.1e-120;
Matches 240; Conservative 0; Mismatches 0; Indels 62; Gaps 1;

OY 82 NTQNSIVSTRSTKKLLRNMDEQASIDYLSNOVETLMNRVLLLTTEVFRKQLODFPHR 141
DB 1 ntqnsivstrstkkllrnmdeqasidylsnqvnelmrvlllttevftrkqlpdpfphr 60
OY 142 PVQSHGLDCTDIKDTIGSVTKTPSGLYITHPGSSYPFEVMCDMDYRGSGWTVIQKRIG 201
DB 61 pvqshgldctdikdtigsvtktpsglyilhpgssypfevmcdmdyrgsgwtvirkridg 120
OY 202 ITDFORLWCMDYLDGFGDLGFEWLGKRTFYVNOKNTSFMLYVALESDDTLAVASYDN 261
DB 121 itdfgrlwcodyldgfgdl----- 139
OY 262 FWLEDETRFRFKHNLGRYSGNAGDAFRGLKKEEDNONAMPSTSDVDNDGCRPACLVNGOSV 321
DB 140 -----gdaftrglkkednampstsdvdndgcrpactlvnqgsv 178
OY 322 KSCSHLHNKTGMWFNECGLANLNGIHNFSGKLLATGICOMGTWKNNSPVKIKSVSKIRR 381
DB 179 kscshlnhktgwmfnecglaingihnfsgkllatgicomgtwknnspvkiiksvsmkirt 238
OY 382 MY 383
DB 239 my 240

RESULT 10
ABG22365
ID ABG22365 standard; Protein: 141 AA.
AC ABG22365;
XX
DT 18-FEB-2002 (first entry)
DB
XX
DE Novel human diagnostic protein #22356.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS86552.

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID No 52724; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 141 AA:

Query Match 30.1%; Score 634; DB 22; Length 141;
Best Local Similarity 64.3%; Pred. No. 3.5e-56;
Matches 119; Conservative 1; Mismatches 3; Indels 62; Gaps 1;

OY 178 PREVMCDMDYRGSGWTVIQKRIDGITDFORLWCMDYLDGFGDLGFEWLGKRTFYVNOK 237
DB 9 prevmcdmdyrgsgwtvirkridgitdfgrlwcodyldgfgdl----- 51
OY 238 NTSFMLYVALESDDTLAVASYDNFWLEDETRFRFKHNLGRYSGNAGDAFRGLKKEEDNONA 297
DB 52 -----gdaftrglkkedn----- 66
OY 298 MPFSTSDVDNDGCRPACLVNGOSVSKSHLHNKTGMWFNECGLANLNGIHNFSGKLLATG 357
DB 67 mpfstsdvdndgcrpactlvnqgsvkshlnhktgwmfnecglaingihnfsgkllatg 126
OY 358 IOWGT 362
DB 127 iqwt 131

RESULT 11
ABG22361
ID ABG22361 standard; Protein: 138 AA.
AC ABG22361;
XX
DT 18-FEB-2002 (first entry)
DB
XX
DE Novel human diagnostic protein #22352.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.

PF	30-MAR-2001; 2001WO-US08631.	
XX		
PR	31-MAR-2000; 2000US-0540217.	
PR	23-AUG-2000; 2000US-0649167.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Dmanac RT, Liu C, Tang YT;	
DR	WPI; 2001-639362/73.	
XX	N-PSDB; AAS86548.	
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
XX	biodiversity -	
PS	Claim 20; SEQ ID No 52720; 103pp; English.	
XX		
CC	The invention relates to isolated polynucleotide (I) and	
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC	and gene mapping, and in recombinant production of (II). The	
CC	polynucleotides are also used in diagnostics as expressed sequence tags	
CC	for identifying expressed genes. (I) is useful in gene therapy techniques	
CC	to restore normal activity of (II) or to treat disease states involving	
CC	(II). (II) is useful for generating antibodies against it, detecting or	
CC	quantitating a polypeptide in tissue, as molecular weight markers and as	
CC	a food supplement. (II) and its binding partners are useful in medical	
CC	imaging of sites expressing (II). (I) and (II) are useful for treating	
CC	disorders involving aberrant protein expression or biological activity.	
CC	The polypeptide and polynucleotide sequences have applications in	
CC	diagnostics, forensics, gene mapping, identification of mutations	
CC	responsible for genetic disorders or other traits to assess biodiversity	
CC	and to produce other types of data and products dependent on DNA and	
CC	amino acid sequences. ABG00010-ABG30377 represent novel human	
CC	diagnostic amino acid sequences of the invention.	
CC	Note: The sequence data for this patent did not appear in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
XX	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SQ	Sequence 138 AA:	
	Query Match 29.9%; Score 628.5; DB 22; Length 138;	
	Best Local Similarity 64.6%; Pred. NO. 1.2e-55;	
	Matches 126; Conservative 1; Mismatches 3; Indels 65; Gaps 1	
QY	1 MMSPOASLFLPNCVLCIFGVEYVQNCVHRHSDSSVYNIIVEGSGNAKDKSNDTYCKED 60	
DB	9 mmsp1a111flfnvcl1fvcgvaqncvshsdcssvvn1vedgnsakdesksndtycked 68	
QY	61 CEESCDVYTKTITREKKEHFCRMIQNSIYSTRSTKLLLNMMDEOQASLDYISNQNELM 120	
DB	69 ceescdvyrktitreekhfnrcmlqnsiysytrstkl1lrnmmdqgasldysng----- 123	
QY	121 NEVLLLTTEVERKKQLDPEPRPVQSHGLDCTDIKDTIGSVTKTPSGLYIIIEGSSYPPE 180	
DB	124 ----- 123	
QY	181 VMCDMDYRGCGWTYL 195	
DB	124 vmcdmdyrg9gwtvl 138	
RESULT 12		
ID	ABG22364	
AC	ABG22364 standard; Protein; 116 AA.	
XX	ABG22364;	
XX		
DT	18-FEB-2002 (first entry)	
XX		

DE	Novel human diagnostic protein #22355.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
RW	food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
PN	WO200175067-A2.
XX	
PD	11-OCF-2001.
PE	30-MAR-2001; 2001WO-US08631.
PR	31-MAR-2000; 2000US-0540217.
PP	23-AUG-2000; 2000US-0649167.
PA	(HYSE-) HYSEQ INC.
PL	Drimanac RT, Liu C, Tang YT;
DR	WPI: 2001-639362/73.
N-PSDB:	AAS86551.
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
PS	Claim 20; SEQ ID No 52723; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Sequence	116 AA;
Query Match	24.8%; Score 521; DB 22; Length 116;
Best Local Similarity	93.1%; Pred. No. 7.9e-45;
Matches	95; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
OY	161 TKTPSGLYIHPEGSSYPEVWCMDYRGCGTWTQKRIIDGIIFQRIMCDYLDFGGDL 220 Db 13 tktpsglyihpegssypewcmcdyrgcgwtvqkridgidfqrimsdyldfggdlv 72 OY 221 GFENGLTKRTFYVNOKNTSFMILVALSESDDTLAYASDNF 262 Db 73 gfenlgtlkrtfyvnokntsfmilyvalsesddtlayasdnf 114 RESULT 13 AAAY26196 ID AY26196 standard; Protein: 491 AA. AC AAY26196;


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PR 19-SEP-1997; 97US-0933821.
XX
XX (GETH ) GENENTECH INC.
XX Botstein D, Ferrara N, Goddard A, Godowski PJ, Gurney AL;
XX Hillan K, Roy M, Schwall R, Tumas D;
XX WPI: 1999-263480/22.
DR N-PSDB; AAX36342.
XX
XX New isolated TIE ligand homologs for, e.g. developing products for
PT treatment of tumors
PS Claim 8: Fig 5; 132pp: English.
XX
XX This sequence is the human tyrosine kinase containing Ig and EGF
CC homology domains (TIE) ligand of the invention, designated N15.
CC The TIE receptors are receptor tyrosine kinases which are expressed in
CC vascular endothelial cells and early haemopoietic cells. The TIE
CC receptors are believed to be actively involved in angiogenesis, and may
CC play a role in haemopoiesis as well. The TIE ligand homologs can promote
CC the survival and/or growth and/or differentiation of TIE receptor
CC expressing cells. They can be used for promoting neovascularisation in
CC wound healing and for promoting angiogenic processes, such as for
CC inducing collateral vascularisation in an ischaemic heart or limb, or for
CC promoting bone development and/or maturation and/or growth in a patient
CC or muscle growth and development. The TIE ligand homologs and antibodies
CC can inhibit the growth of endothelial cells and induce apoptosis of
CC cells, particularly tumour cells. They can inhibit vasculogenesis,
CC particularly the vascularisation of tumour cells. The antibodies can also
CC inhibit vascularisation of a cell in which a gene encoding an N15, N15',
CC N18 or N14 polypeptide is amplified. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic
CC animals.
XX
XX Sequence 491 AA:
SQ

```

```

RESULT 15
AAB24393
ID AAB24393 standard; Protein; 491 AA.
XX
XX AAB24393;
AC
XX
XX 07-NOV-2000 (first entry)
DT
XX
XX Human PRO188 protein sequence SEQ ID NO:26.
DE
XX
XX Human: PRO: promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiac; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO200032221-A2.
PN
XX
XX 08-JUN-2000.
PD
XX
XX 30-NOV-1999; 99WO-US28313.
XX
XX 01-DEC-1998; 98WO-US25108.
PR 16-DEC-1998; 98US-0112850.
PR 12-JAN-1999; 99US-0115554.
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-OCT-1999; 99US-0162506.
XX
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ, Goddard A;
XX Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF, Smith V;
XX Watanabe CK, Williams PM, Wood WI.
XX
XX WPI: 2000-412154/35.
DR N-PSDB; AAA77529.
XX
XX Nucleic acids encoding PRO polypeptides useful for preventing,
PT diagnosing and treating disorders a cardiovascular, endothelial or
PT angiogenic disorders in mammals -
XX
XX Claim 72: Fig 12: 315pp: English.
XX
XX The present invention describes nucleic acids encoding PRO polypeptides
XX useful for preventing, diagnosing and treating disorders in mammals by
XX cardiovascular, endothelial or angiogenic disorder in mammals by
XX modulating cell proliferation, angiogenesis and cardiovascularisation,
XX and for identifying agonists and antagonists of these processes. The
XX nucleic acids and the proteins they encode may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate PRO expression such as cardiovascular, endothelial or
XX angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
XX cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors
XX containing them and the PRO polypeptide may be used to treat disorders
XX associated with decreased PRO expression. AAA77510 to AAA77721 and
XX AAB24388 to AAB24435 represent nucleotide and protein sequences used in
XX the exemplification of the present invention.

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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:05:08 ; Search time 22.62 Seconds
(Without alignments)
418.971 Million cell updates/sec

Title: US-09-596-196-4
Perfect score: 2104
Sequence: 1 MMSPSOAFLFNWCFICG.....PVKIKSVSMKIRMYNPFYK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6CTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	20.2	491	2	US-08-933-821-4
2	425	20.2	491	3	US-08-960-507-4
3	425	20.2	491	4	US-09-136-828-4
4	405.5	19.3	490	4	US-08-740-223A-12
5	403.5	19.2	497	4	US-08-740-223A-4
6	402.5	19.1	497	1	US-08-373-579-4
7	402.5	19.1	497	2	US-08-418-595-4
8	402.5	19.1	497	2	US-08-665-926-4
9	402.5	19.1	497	2	US-08-348-492-4
10	402.5	19.1	497	2	US-09-162-437-4
11	400	19.0	493	2	US-08-933-821-2
12	400	19.0	493	3	US-08-960-507-2
13	400	19.0	493	4	US-09-136-828-2
14	399	19.0	492	1	US-08-525-505A-4
15	395.5	18.8	496	4	US-08-740-223A-22
16	395	18.8	478	4	US-08-740-223A-7
17	395	18.8	495	4	US-08-740-223A-26
18	395	18.8	498	4	US-08-740-223A-2
19	395	18.8	498	4	US-09-351-457-2
20	395	18.8	498	4	US-09-561-500-2
21	395	18.8	498	4	US-09-561-108-2
22	394	18.7	495	4	US-09-351-457-5
23	394	18.7	495	4	US-09-561-500-5
24	394	18.7	495	4	US-09-561-108-5
25	393	18.7	491	4	US-08-740-223A-13
26	389	18.5	314	1	US-08-525-505A-2
27	389	18.5	498	1	US-08-373-579-2

28	389	18.5	498	2	US-08-418-595-2	Sequence 2, Appl1
29	389	18.5	498	2	US-08-665-926-2	Sequence 2, Appl1
30	389	18.5	498	2	US-08-348-492-2	Sequence 2, Appl1
31	389	18.5	498	4	US-09-162-437-2	Sequence 2, Appl1
32	387.5	18.4	497	4	US-08-740-223A-14	Sequence 14, Appl1
33	381.5	18.1	480	4	US-08-740-223A-8	Sequence 8, Appl1
34	381.5	18.1	496	1	US-08-373-579-6	Sequence 6, Appl1
35	381.5	18.1	496	2	US-08-418-595-6	Sequence 6, Appl1
36	381.5	18.1	496	2	US-08-665-926-6	Sequence 6, Appl1
37	381.5	18.1	496	4	US-09-162-437-6	Sequence 6, Appl1
38	381.5	18.1	496	4	US-08-740-223A-6	Sequence 6, Appl1
39	381.5	18.1	496	4	US-09-351-457-4	Sequence 4, Appl1
40	381.5	18.1	496	4	US-09-561-500-4	Sequence 4, Appl1
41	381.5	18.1	496	4	US-09-561-108-4	Sequence 4, Appl1
42	381.5	18.1	499	4	US-08-740-223A-24	Sequence 24, Appl1
43	381	18.1	498	4	US-08-740-223A-20	Sequence 20, Appl1
44	380	18.1	346	3	US-08-960-507-19	Sequence 19, Appl1
45	375.5	17.8	491	1	US-08-206-176-4	Sequence 4, Appl1

ALIGNMENTS

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RESULT 1
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-933-821-4

Query Match 20.2% Score 425; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 1e-35;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

QY 44 SNAKDESKNDYCKKCECSQVYKTYRE-EKHEVCRLNLSIYSTSTKLLRNMM 102
Db 68 TKQDASTITDMTRMDLENLKVLSRKQREIVLQVVDGNIYNEVLLKRESNNM 127
QY 103 DE-QQASLDLY-----SNOVNEIDMNRVLLITTE----- 129
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Db	128	SRVQLVQLLHEIIRKADNSLELSQENKILAVTTTEMLKATRYRELEKVASLDTLVN	187
QY	130	-----VRRKQ---LDP-----FHRPVQSHGL-----	148
Db	188	NQSWITLLLEEOLRIETSRDOTHVSPRLVQVVRPHNIENSOOYFPPGLGNEIDQDPGPR	247
QY	149	DCDILKDIIGSVTKTP-----SGLTIIHPGSSYFEV	181
Db	248	DLMPPLDPTSPYSPEKIPRPVTEINEGPRKCOQAK EAGHSVSGIYMKPENSNGPMQL	307
QY	182	MCDMDYRGCGVTVIOKRDIIDFQRLMCDVLDGFDGLGFEMLKIFVYIQKPTSF	241
Db	308	WCENSLDPGCGTVIOKRDKGSVNFRRNNKNTKKKGFQINIDGFTYGLGENTYMLSNQDN--Y	365
QY	242	MLVVALESEDITLVAASYDNFMLEDETEFFFKMIGRGYSNGNAGDAFRGLAKREDNONAMPFS	301
Db	366	KLIIIELEDMDSKKVYAEVSFRLEPESFPYLRGLGTQGNANQDMMN-----HNGKQFT	419
QY	302	TSVDVNDGCRPACLVNGOSVKSCHLHNKTKGMFNEBEGLANLNGIHHPSGKLLA--TGI	358
Db	420	TLDPRKD-----MYAGNCANHF-KFGGMWYNACASHNLNGLVWYRGCHYRSKHODGI	468
QY	359	QMGTMTKNNSPVKTIKSVSMKR	380
Db	469	FMAEY--RGGSYSLRAVOMMTK	488

RESULT 2
 US-08-960-507-4
 : Sequence 4, Application US/08960507
 : Patent No. 6057435
 : GENERAL INFORMATION:
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Gurney, Austin L.
 : TITLE OF INVENTION: The Ligands
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPatIn (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/960.507
 : FILING DATE:
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Dreyer, Ginger R.
 : REGISTRATION NUMBER: 33,055
 : REFERENCE/DOCKET NUMBER: P1130p1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650/225-3216
 : TELEFAX: 650/952-9881
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 491 amino acids
 : TYPE: Amino Acid
 : TOPOLOGY: Linear
 :
 : US-08-960-507-4

	Query Match	20.2%	Score 425;	DB 3;	Length 491;
	Best Local Similarity	26.9%	Pred. No. 1e-35;		
	Matches 119; Conservative	64;	Mismatches 133;	Indels 126;	Gaps 14;
Q7	44 SNAKESNDIVCEDEECSDVYTKITRE-EKHFMCNLONLSIVSYRSTKRLLRNMM	102	:	:	:
	: : : : : :	:	:	:	:
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Db      128  SRVQLVWQLHEIIRKRDNSLELSQENKILNVTYEMLKATRYRELEVYASLTDLVN 187
QY      130  -----VERKQ---LDP-----PFRPVQSHGL----- 148
Db      188  NQSVMTLLEBQCLRIEFSRQDTHVSPRLVQVPRQHIINPSQUTYRGLLGGNEIORDPGR 247
QY      149  DCTDIKDTIGSVYTP-----SGLYTHPESSVPFEV 161
Db      248  DLMPPRLDATSPKSPFKIPVPTFINEGRFKDCQAKESCHVSGIATYMKPENSNGPMQL 307
QY      182  MCDMDYRGCGTIVIQKRLDGIIDQRLMCDYLDGFGDLSEFYLGLKITYYVQKQTSF 241
Db      308  WCENSLDPGCGTIVQKRTDGSVNFPEFRMWNENYKCGFNIDDEYWLGLENIYMLSDON--Y 365
QY      242  MLYVALESEDDTLAVASVDNFMLEDETRFRFMHLGRSGNAGQAFRLKKEDONAMPFS 301
Db      366  KLLIELEWDSOKKYVAEYSSFRLESEFEYRLIRGTQVGNAGSMMV-----HNGKPT 419
QY      302  TSDVDNDCRPACLVNGQSVKSCSHLNNKTCGMWNEEGCLANLUNGIIHFSKGLA--TGI 358
Db      420  TLDLRDKD-----MYAGNCNHFH-KGGWYNACASHSLNGLNVMYRGCHYRSKHODGI 468
QY      359  QMGTYTNNKNSPVKIKSVSMKIR 380
Db      469  FWAELY--RGGSYSILRAVQMMIK 488

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RESULT 33
 US-09-136-828-4
 Sequence 4, Application US/091366828
 Patent No. 6350450
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: Tle Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136, 828
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Ginger R.
 REGISTRATION NUMBER: 33, 055
 REFERENCE/DOCKET NUMBER: P1130X1A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 491 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-136-828-4

Query Match	20.28;	Score 425;	DB 4;	Length 491;
Best Local Similarity	26.98;	Pred. NO. 1e-35;		

	Matches	119;	Conservative	64;	Mismatches	133;	Indels	126;	Gaps	14
Oy	44	SNAKESBSNDTVCKEDECDESDCVTKITRE- EKHPRMCNLONSIVSTRSTKLLRNMM	102							
Db	68	TKGDASATIKMITRMDLENELKLDVLSROKREIDVLQLVVDGGINVNEVKLLRESRRNN	127							
Oy	103	DE-QDASLDYL-----SNQVNELMNRVLLTTE	129							
Db	128	SRVQVLVQMLHEITRKRDNSLELSOLENKILNVTTTEMLKMATRYRELEVYASLTDLVN	187							
Oy	130	-----VFRKQ--LDP-----PRRPRVOSHGL-----	148							
Db	188	NQSVMITLLEEOCLRFSSKODTHNVSPREYOVYVPHNIPNSQOYTLPGLLGNEIQRDPGYPR	247							
Oy	149	DCDTIKDITIGSTYKTR-----SGLYIITHPGSSYPRFV	181							
Db	248	DLMPRPDLATSTKSKPRKPIRYPTFINEGRFFCKOQAKEGHSVSGIYMKKPKPENSNGPRMOL	307							
Oy	182	MCDMDYRGSGWTVIOKRIIDGIDIFORLWCDYLDGFGDILGEBFLGSLKFTYIVNOKNTSE	241							
Db	308	WCENSILDRGGWTVIOKRTGDSVNFPRNMWNTYKKKFGNIDGEEWGLGENTYMLSNODN--Y	365							
Oy	242	MIYVLESEBDOTLAAASYDNFWLEDETREFKNHLGRYCSGNADDAFRGLKKEKNQNMMPRS	301							
Db	366	KLLILEMWSDKKVAEYSSFRLEPSESEYRIURLGYGOSNADDSMMW-----HNGKQFT	419							
Oy	302	TSVDVNDGCRPACLYANGOSVSKSCSHLHNHTGWMFNECGLANGLNGIHNFSGKLTA--TG1	358							
Db	420	TLDRODKD-----MYAGNCANFH--KGMWVYNACANSLNGLNVYRGCHYKSKHQDGI	468							
Oy	359	OMGTWTKNNSPYKIKSVSKIR	380							
Db	469	PWAEEY--RGGSYSLRAYVQMMIK	488							

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1 RESULT
2 US-08-740-223A-12
3 ; Sequence 12, Application US/08740223A
4 ; Patent No. 6265564
5 ;
6 ; GENERAL INFORMATION:
7 ; APPLICANT: Davis, et al.
8 ; TITLE OF INVENTION: Expressed Ligand - Vascular
9 ; TITLE OF INVENTION: Intercellular Signalling Molecule
10 ; NUMBER OF SEQUENCES: 28
11 ;
12 ; CORRESPONDENCE ADDRESSES:
13 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
14 ; STREET: 777 Old Saw Mill Road
15 ; CITY: Tarrytown
16 ; STATE: NY
17 ;
18 ; COUNTRY: USA
19 ;
20 ; ZIP: 10591
21 ;
22 ; COMPUTER READABLE FORM:
23 ; MEDIUM TYPE: Diskette
24 ; COMPUTER: IBM Compatible
25 ; OPERATING SYSTEM: DOS
26 ; SOFTWARE: FastSEO version 2.0
27 ;
28 ; CURRENT APPLICATION DATA:
29 ; APPLICATION NUMBER: US/08/740.223A
30 ; FILING DATE: 25-OCT-1996
31 ; CLASSIFICATION: 536
32 ;
33 ; PRIOR APPLICATION DATA:
34 ; APPLICATION NUMBER: USSN 60/022/999
35 ; FILING DATE: 02-AUG-1996
36 ;
37 ; ATTORNEY/AGENT INFORMATION:
38 ; NAME: Cobert, Robert J
39 ; REGISTRATION NUMBER: 36,108
40 ; REFERENCE/DOCKET NUMBER: REG 333
41 ; TELECOMMUNICATION INFORMATION:
42 ; TELEPHONE: 914-345-7400
43 ; TELEFAX: 914-345-7721
44 ;
45 ; INFORMATION FOR SEQ ID NO: 12:
46 ;
47 ; SEQUENCE CHARACTERISTICS:
48 ;
49 ; LENGTH: 490 amino acids

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:      TYPE: amino acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:      MOLECULE TYPE: protein
:      FEATURE:
:      NAME/KEY: hTTL
:      LOCATION: 1...490
:      OTHER INFORMATION: human TIE-2 ligand 1
:      OS-08-740-223A-12

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Query Match	19.3%;	Score 405.5;	DB 4;	Length 490;
Best Local Similarity	27.5%;	Pred. No. 1.1e-33;		
Matches 118;	Conservative 65;	Mismatches 125;	Indels 121;	Gaps 16;

OY	23	VOCNHVSTSDSVVNIVEDGSNKNDEKSDNDYVCSKEDCESSOYVTKTRIRREKNHFCRN	82
Db	108	IOONAVONHNT-----ATMLEISTSLLSOT-----AEOTKRLDVETOVLNQSREIOL	156
OY	83	LONISVY-----TRSTKPLRNMM	102
Db	157	LENSLSTYKLEKLOOTNEILKTHEKSNLLEHKLILEMEGKHKEDELDTLKEEKNLOGLV	216
OY	103	DEQASLDYLSNOVN-----ELM-----NRVLLTTEYV-----EKODPEP	139
Db	217	TRQTYIIIOELERKOLNRAATTNNSVLQKOOLEIMDTVHNLVNLCTKEVLLKSGKKEEKEP-	275
OY	140	HRPVQSHGLDSTDIDKDTIGSTVTKPSGLYIIHPREGSSYPPEVMCDMDYRGCGMTVIOKRI	199
Db	276	-----RDCADVY-----QNGFKKSGIYTIYINMPEPKKVCFCNMVYNGCGMTVIOHRE	323
OY	200	DOIDFORLWCDYLDGEGDLDGEFMLGLKIEYIVNOKNTPFMYALVESEDDTLAYAST	259
Db	324	DGSDLEFORGMKEYKMGFEFNPSGGEYWLGNIEFFAITSOR--OYMLRIELAMEGKNRAVSQY	381
OY	260	DNFWEDEDTREFKFNHLGYSGNADDAFNGLKEDN--QNMNPSTSDVYNDGCRPAC--L	315
Db	362	DREHIGNKONTRLKLTGHTAG-----KQSSLLHIGADSTKADNDNCKSCALM	424
OY	316	VNGOSVKSCHLHNKGMWFNEEGCLANLNGIHNS-----GKLATGJQWNGTWTKNNSPVK	371
Db	435	LIG-----GWMFADCGPSNLNGMEFYTAGQNHGKL--NGIKMHWY--KGPSYS	477
OY	372	IKSVSMKTR	380
Db	478	IRSTTMMIR	486

RESULT 5
 US-08-740-223A-4
 Sequence 4, Application US/08740223A
 Patent No. 6265564
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 TITLE OF INVENTION: Intracellular Signalling Molecule
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill Road
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/740, 223A
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 536

OY 372 IKSYSMKIR 380
Db 485 LRSTTMMIR 493

RESULT 7
US-08-418-595-4
; Sequence 4, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595
; FILING DATE: 06-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,932
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; TELEFAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-418-595-4

Query Match 19.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 2.3e-33;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

OY 23 VQNCVHHSTDSVYNIVEDGSKNDVCKEDCESCDVKITREKHFMCN 82
Db 115 IQQNAVQNHNT-----ATMLEIGTSLSQ-----AEQTRKLTGVENQVLNQTSLRIQL 163
OY 83 LQNSIVS-----TRSTKLLRMM 102
Db 164 LENSLSYTKLEKOLLQOTNELIKHEKNSLLEHRILEMEGKHKEELDTLKEKEKNLQGLV 223

OY 103 DEQASLDYLSNOVN-----ELM-----NRVLLTTEVE-----RKOLDPEP 139
Db 224 TRQTYITIOLEKOLNRAFTNNSVLQKOOLEMDVHNLNCTKEVALLGKGRREDDPF 282
OY 140 HRPVOSHGLDCTDIKRTGVTSPGLYIIRPEGSYPFEVWCDMDYRGCGVTIOKRI 199
Db 283 -----RDCADYV-----QAGFNKSGIYTYIINMPEPKKVFPCNMVNGGMYVIOHRE 330
OY 200 DGIIDFQRLMCDYLDGFGDGLGEFVLGKRTFYIVNOKNTSFMILYVLESDDTLAYASY 259
Db 331 DGSIDFQRMKEVYMGFGNPSGEYWLGNFTFATTSOR--QYMLRIELMDGEMRAVSQY 388
OY 260 DNFMLEDTRFEKMHILGRYSGNAGDAFRGKEDN--QNAFPSTSDVNDGCRPAC--L 315
Db 389 DRFHIGNEKQYRKLXKGHTAG-----KQSSLIHGADFSTKADNDNCCKKCALM 441
OY 316 VNGOSVNSCSHLHNTGWFNEGILANLNGIHES---GKLATGIIQWGTWTRNNSPVK 371
Db 442 LTG-----GWFADACGPNLNGMFTYAGQNHGKL--NGIKMYF--KGRSYS 484
OY 372 IKSYSMKIR 380
Db 485 LRSTTMMIR 493

RESULT 8
US-08-665-926-4
; Sequence 4, Application US/08665926
; Patent No. 5851797
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al.
; TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,926
; FILING DATE: 19-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert J. Cobert
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 330-H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-2113
; TELEFAX: (914) 345-7400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-665-926-4

Query Match 19.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 2.3e-33;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

OY 23 VQNCVHHSTDSVYNIVEDGSKNDVCKEDCESCDVKITREKHFMCN 82
Db 115 IQQNAVQNHNT-----ATMLEIGTSLSQ-----AEQTRKLTGVENQVLNQTSLRIQL 163

```

QY      83  LONSIVS-----TRSTKLLRNM 102
Db      164  LENSISTYKLEKOLLQOTNELTKIHEKNSLLEHKILEMECKIHKEDDTLKEKENIQLGY 223
QY      103  DEQASIDLYSNOVN-----ELM---NRVLLTTEVF---RKOLDPEP 139
Db      224  TRQYIIIOLELEKQOLNRATNTNSVLOKQOLEIMDTVMNLVLCFKEVLLKGGKREEDKPF- 282
QY      140  HRPVSHGLDCTDILKPIIGSTKTRPSLLYIIHPGSSYPPEWCOMDQYRCGGTIVYQKRI 199
Db      283  -----RDCADYV---QAGFNKSGIYTYIINNPEPKVFCNMDVNGGWTIVYQHRE 330
QY      200  DGIIDFQRLMCDYLDGFGDILLGEFWLKLKIFYIVNOKNTSFMLYVAJESEDTLAVASY 259
Db      331  DGSIDFQGWKEYEMKMGNGNPSGEVWLONEFIFATTSQR--QYMLRIELMDEGNRAYSQY 388
QY      260  DNFWELEDFTRFKMHLGRYSGNAGDAERGLKEDN--QNMPPSTSDVDNDGCRPAC--L 315
Db      389  DRFHIGNEKQVRYRLYLKXHGHTAG-----KQSSILLHGADEFSTKPDADNDCMCCALM 441
QY      316  VNGQSVKSCSHLHNKGTGWPEEGCLANTNGIHHS---GKLATGDMGTWTKNNSPVK 371
Db      442  LTG-----GMPFACGSPNSLNGMEYTAGONHGKL--NGIKWHYF--KGPSYS 484
QY      372  IKSVSMKIR 380
Db      485  LRSTTMMIR 493

RESULT      9
US-08-348-492-4
: Sequence 4, Application US/08348492
: Patent No. 5879672
: GENERAL INFORMATION:
: APPLICANT: Davis, et al.
: TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/348,492
: FILING DATE: 02-DEC-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/330,261
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/319,932
: FILING DATE: 07-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Kempier, Gail M.
: REGISTRATION NUMBER: 32,143
: REFERENCE/DOCKET NUMBER: REG 330B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 347-7000
: TELEFAX: (914) 347-2113
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 497 amino acids
: TYPE: amino acid
: TOPOLOGY: linear

```

[illegible]

FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coberl, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-4

Query Match 19.1%; Score 402.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No. 2,3e-33;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

23 VQNCVHHSTDSVVNIIVDGSNAKDESKNDVCKEDCESCDVYKTRREKHPMCRN 82
115 IQQNAVQNT-----ATMEIGTSLSQT-----AEQTRKLDVETQVLYNQTSRLIEDL 163
83 LQNSIVSY-----TSTTKILLRNMA 102
164 LENSISTYKLEKQLQOQTNEILKHEKNSLLEKILMEGKHKEEDLTKEEKENLGVLV 223
103 DQOASLDVLSQNVN-----ELM-----NRVLLLTVEF-----RKQIDPPR 139
224 TQOTYIIQLEKQLNATNTNSVLOKQOLEMDTVHNLVNLCTKEVLLKGKREEDKPR- 282
140 HRPVOSHGLDCTDIKDTIGSVTKPSGLYIHPREGSSYFEVMDYRGSGWTYQKRI 199
283 -----RDCAADV-----QAGFNKSGITTYIINNMPERKAYPCNMDVAGGCTVYQHNE 330
200 DGIIDFQRLMCDYLDGEGDLLGEFWLGLKRFIYVNOKNTSFMLYVALESEDOTLAASY 259
331 DGLDFQRCMKKEKMGFGNPGEYWLGNFEIFAITSOR--QYVLRLELMDMEGNRAYSQY 388
260 DNEWLEDERFRFKMHLGRYSNAGDAFRGLKEDN--QANAMPSTSDVDNDGCRPAC--L 315
389 DRFHIGNEKQNTRLYKLGKGTAG-----KQSSLLHGADESTKDADNDNCMCALM 441
316 VNGQSVKSCSHLHNTGWMFNEGCLANGLIHFS---GKLLATGIQMGWTKNNSPVK 371
442 LRG-----GWFDAQCGPSNLGMFTYTAGNNGKL--NQIKKHVF--KQPSYS 484
372 IKSVMKIR 380
485 LRSTTMMIR 493

RESULT 11
US-08-933-821-2
Sequence 2, Application US/08933821
Patent No. 5972338
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,821
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-933-821-2

Query Match 19.0%; Score 400; DB 2; Length 493;
Best Local Similarity 31.9%; Pred. No. 4,2e-33;
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

117 NELMNRVLLLTTEVFRKQ-----LDPPRRPVQSHGLDCTDIKDTIGSVTKPSG----- 166
231 NRIINQI--STNEIQSDQMLKVLPPPLPTMPTLT-----SLPSSIDKPSGWRDC 278
167 -----LYIHHPREGSSYFEVMDYRGSGWTYQKRIIDTDFQRLMCDYLD 214
279 LQALEDHDTSSLYLVKRPENTNRLMQWCDQRHDPGQVTVIORLDGVSYFRMMEYTKO 338
215 GFCDLLGEFWLGLKRFIYVNOKNTSFMLYVALESEDOTLAASYDNFMLEDETRFKMH 274
339 GGNIDGCEYWLGLENTYWLTLQGN--YKLLVTMEDMSGKRVAREYASFLEPSEYTKLR 396
275 LGRYSNAGDAFRGLKEDNQNAMPSTSDVDNDGCRPACLVNGQSVKSCSHLHNTGMW 334
397 LGRYHGNAGDSFTW-----HNGKQFTLDRDHD-----VYTG---NCAH-YQKGMW 439
335 FNEGCLANGLIHHPGSKLLA---TGIONGTWTKNNSPVKIKISVSKIRMTNPNY 386
440 YNACAHSNLNGVWYRGHYRSRYQGVYAAEF--RGGSYSLKRVYVMIRPNPTF 492

RESULT 12
US-08-960-507-2
Sequence 2, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-960-507-2
```

Query Match 19.0%; Score 400; DB 3; Length 493;

Best Local Similarity 31.9%; Pred. No. 4.2e-33; Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

```
OY 117 NELMNRVLLTTEVFRKQ-----LDPPRHRVQSHGLDCTDIKDTIGSVTKTPSG----- 166
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 231 NRIINQI--STNETISDQNKLVLPPLPTMTLT-----SLPSTDKPGGPRDC 278
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 167 -----LYIHPESSYFEVWCDMDYRGGMVYQKRIDGIIDFORLWCDYLD 214
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 279 LQLEDGHDTSITLVPEPNTNRLMQWCDORHPGGMVYIQRLDGSVNEFRMWTYKQ 338
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 215 GFGDLGEFVLGKIKIYIYNQKNTSFMLYALESEDDTLAASYNFMWLEDETRFFKM 274
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 339 GFGNIDSEYMLGLENITWLTNQG--YKLLVTMEDMGSRKFAEYASFRLEPESEYKLR 396
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 275 LGRYSNAGDAFRGLKEDNOMAPFSTSDVNDGCRPACLVNGQSVKSGSHLNKTKGMW 334
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 397 LGRYHGNAGSEFTW-----HNGKQFTLLDRDHD-----VYTG-----NCAH-YQKGGW 439
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 335 FNEGCLNGLNGIHHSGLKLA--TGIGMGWTNKNSPVKIKSVKIRRMVNPY 386
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 440 YNCAHSLNGLVWYRGHYSRYODGYVMAEF--RGGSYSLLKVKVMIRPNPNTF 492
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 13

```
US-09-136-828-2
Sequence 2, Application US/09136828
Patent No. 6350450
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: The Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,828
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130R1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-136-828-2
```

Query Match 19.0%; Score 400; DB 4; Length 493;

Best Local Similarity 31.9%; Pred. No. 4.2e-33; Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

```
OY 117 NELMNRVLLTTEVFRKQ-----LDPPRHRVQSHGLDCTDIKDTIGSVTKTPSG----- 166
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 231 NRIINQI--STNETISDQNKLVLPPLPTMTLT-----SLPSTDKPGGPRDC 278
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 167 -----LYIHPESSYFEVWCDMDYRGGMVYQKRIDGIIDFORLWCDYLD 214
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 279 LQLEDGHDTSITLVPEPNTNRLMQWCDORHPGGMVYIQRLDGSVNEFRMWTYKQ 338
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 215 GFGDLGEFVLGKIKIYIYNQKNTSFMLYALESEDDTLAASYNFMWLEDETRFFKM 274
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 339 GFGNIDSEYMLGLENITWLTNQG--YKLLVTMEDMGSRKFAEYASFRLEPESEYKLR 396
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 275 LGRYSNAGDAFRGLKEDNOMAPFSTSDVNDGCRPACLVNGQSVKSGSHLNKTKGMW 334
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 397 LGRYHGNAGSEFTW-----HNGKQFTLLDRDHD-----VYTG-----NCAH-YQKGGW 439
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 335 FNEGCLNGLNGIHHSGLKLA--TGIGMGWTNKNSPVKIKSVKIRRMVNPY 386
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 440 YNCAHSLNGLVWYRGHYSRYODGYVMAEF--RGGSYSLLKVKVMIRPNPNTF 492
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 14

```
US-08-525-505A-4
Sequence 4, Application US/08525505A
Patent No. 5807711
GENERAL INFORMATION:
APPLICANT: HARA, HIROSHI
APPLICANT: YOSHIMURA, HIROMITSU
APPLICANT: MATSUKI, YUMIKO
APPLICANT: SHINDO, SAEKO
APPLICANT: HANADA, KAZUNORI
TITLE OF INVENTION: PARENCHYMAL HEPATOCYTE GROWTH SUBSTANCE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,505A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/JP94/00455
FILING DATE: 22-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-063905
```

FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: OHLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-505A-4

Query Match 19.0%; Score 399; DB 1; Length 312;
Best Local Similarity 34.3%; Pred. No. 2.6e-33;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 87 IVSTYSTRKLLRNMDDEQASLDYLSNOYNEIMNRVLLITTEVERKQ-----134
DB 4 VFSFIIIVTVALI--MGREISALEDCAQEQMRRAQVRLLETHVKQOQVXIKOLQENEV 60
QY 135 --LDPPFHPVQSHG-----LDCTDIKDTIGSVTKTPSGLYIHPRESSVPFEWCDMDY 187
DB 61 QFLDKGDENTVDLGSRKQYADCELFNDGYKL---SGFYKIKPLQSPAEFSYCDMS- 115
QY 188 RGGGWTVYQKRIQIDIFDLQFMDYLDGFGDL--GEFWLGLKIFYIVNOKNTSEMLY 244
DB 116 DGGGWTVYQKRSQSEFNNGMKGWYENGFGNFYQKHGEYVLGNKLNHLFTQED--YTLK 173
QY 245 VALESDDTAYVSYDNFWELEDETRFKMHLGRYSGNAGAFGLKKEDNQ-----NAMP 299
DB 174 IDLADEKKNRYAQKFKFKYDEKNEFELNIGESGTAGDSLGNFHPDEVQWMAHQRMK 233
QY 300 FSTSDVNDGCRPACLYNGSVKSCSHLNKGMWNEGCLANLNGIHHSKLLA---T 356
DB 234 FSTWDRDHDYEGNCAEEDS-----GWFNRCHSANLNGV--YSGPYTAKTN 281
QY 357 GIQMGTWTKNNSPVKIKSVSMKIR 380
DB 282 GIWWTW--HGMWYSLKSVYMKIR 303

RESULT 15
US-08-740-223A-22
Sequence 22, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999

FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: 2N2C1F (chimera 2)
LOCATION: 1...496
OTHER INFORMATION:
US-08-740-223A-22

Query Match 18.8%; Score 395.5; DB 4; Length 496;
Best Local Similarity 27.5%; Pred. No. 1.2e-32;
Matches 116; Conservative 68; Mismatches 133; Indels 105; Gaps 17;

QY 23 VQGNCHVHSTDSVYVNIIVEDGSKNAKDESKNDYVKEDECESDVYTKI---TREE--- 75
DB 112 IQONAVNQOT---AWMIEIGTNLNOT-----AEQTRKLDVEAOVLYNQTTRELTQL 160
QY 76 -KHFMGN-LQNSTIVSTRSTKTL-----LNNMDEQASL 109
DB 161 LEHSLSTNKLKQIQLDQTSINKLQDKNSFLKVKLAMEDKHITQLOSTIEEKQDQVLY 220
QY 110 DYLSNOYNEIMNRVLLIT--TEVERKQ-----LDPPFHPVQSH 146
DB 221 SKQNSIIELEKKIVTATVANSVLQKQOHDLMETVNNLLTMSTSNASKAPYAKKEQIS 280
QY 147 GLDCTDIKDTIGSVTKTPSGLYIHPGSSYPFEWCDMDYRGGGWTVYQKRIQIDIFQ 206
DB 281 FRCDADYV---QAGFNKSGIYIYINNMPKPKVFCNMDVNGSGWTVYQKHREDGSLDFQ 336
QY 207 RLMCDYLDGFGDLGGEFWLGLKIFYIVNOKNTSEMLYVALESDDTAYVSYDNFWELE 266
DB 337 RGMKEYKMGFNPDSGEYWLGNFETFAITSOR--QYMLRIELMDEGKRAISQYDRFHIGN 394
QY 267 ETRFEKMHILGRYSGNAGDAFRGLKKEDN--QNAMPSTSDVNDGCRPAC--LVNGOSVK 322
DB 395 EKQYRRLYLKGHGTAG-----KQSSLLHGADEFSTKDADNDNCMKCALMLTG---- 443
QY 323 SCSHLNKGTWNEGCLANLNGIHHS---GKLTATGIQMGTWTKNNSPVKIKSVSMK 378
DB 444 -----GWFPDACPSNLNGWFTYAGONHGKL--NGIKWYF--KGPSYSLRSTYTM 490
QY 379 IR 380
DB 491 IR 492

Search completed: May 22, 2002, 15:07:54
Job time: 166 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:13:50 ; Search time 17.4 Seconds
(without alignments)
818.896 Million cell updates/sec

Title: US-09-596-196-9
Perfect score: 2000
Sequence: 1 EVVQNCVHSTDSVNVIV.....PVKIKSVSMKIRMYNPER 368

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 segs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	413.5	20.7	439	1	FGL2_HUMAN
2	405.5	20.3	432	1	FGL2_MOUSE
3	400.5	20.0	431	1	AGP1_BOVIN
4	400.5	20.0	493	1	ANL2_MOUSE
5	400.5	20.0	493	1	ANL2_HUMAN
6	398.5	19.9	312	1	FGL1_HUMAN
7	395.5	19.8	468	1	FIBB_BOVIN
8	391.5	19.6	498	1	AGP1_HUMAN
9	381.5	19.1	496	1	AGP2_MOUSE
10	375.5	18.8	491	1	FIBB_HUMAN
11	375.5	18.8	375	1	AGP2_BOVIN
12	374.5	18.7	496	1	AGP2_MOUSE
13	373.5	18.7	479	1	FIBB_RAT
14	371.5	18.6	463	1	FIBB_CHICK
15	370.5	18.5	477	1	FIBB_PETMA
16	367.5	18.4	453	1	FIBG_BOVIN
17	365.5	18.2	444	1	FIBG_BOVIN
18	360.5	18.0	432	1	FIBG_PETMA
19	360.5	18.0	509	1	AGP4_MOUSE
20	358.5	17.9	503	1	AGP4_HUMAN
21	352.5	17.6	438	1	FIBG_XENLA
22	351.5	17.6	319	1	FCN2_RAT
23	350.5	17.5	782	1	FIBA_PARPA
24	348.5	17.4	724	1	SCA_DROME
25	337.5	16.9	866	1	FIBA_HUMAN
26	335.5	16.8	741	1	FIBB_CHICK
27	332.5	16.6	306	1	FCN2_MOUSE
28	329.5	16.5	641	1	FIB2_PETMA
29	329.5	16.4	334	1	FCN1_MOUSE
30	327.5	16.4	445	1	FIBG_RAT
31	321.5	16.1	313	1	FCN2_HUMAN
32	321.5	16.1	255	1	MF4_HUMAN
33	321.5	16.1	255	1	MF4_HUMAN

34	313.5	15.7	782	1	FIBA_RAT	P06399
35	310.5	15.5	1808	1	TENA_CHICK	rattus norv
36	305.5	15.3	335	1	FCN1_RAT	P10039
37	303.5	15.2	326	1	FCN1_HUMAN	gallus gall
38	302.5	15.1	4289	1	TENX_HUMAN	O9wts8
39	291	14.6	299	1	FCN3_HUMAN	rattus norv
40	282.5	14.1	1746	1	TENA_PIG	P22105
41	271	13.6	2201	1	TENA_HUMAN	homo sapien
42	197	9.8	137	1	AGP2_RAT	O75636
43	109	5.5	129	1	MF4_BOVIN	homo sapien
44	98	4.9	782	1	BICD_DROME	O29116
45	97.5	4.9	1432	1	SKI3_YEAST	mus scrofa

ALIGNMENTS

RESULT 1
FGL2_HUMAN FGL2_HUMAN STANDARD: PRT; 439 AA.
ID FGL2_HUMAN Q14314:
AC Q14314:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibrinogen-like precursor (Fibrinogen-like protein 2) (P149).
GN FGL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=95369700; PubMed=7642106;
RA Ruegg C., Pyela R.;
RT "Sequence of a human transcript expressed in T-lymphocytes and encoding a fibrinogen-like protein."
RL Gene 160:257-262(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Yuwara J S., Liu M., Marsden P., Levy G.;
RT "Cloning and characterization of FGL2, the human counterpart to the mouse gene Fgl2."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION:
RX MEDLINE=98309432; PubMed=9647217;
RA Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA Arraraves S., von Fliedner V., Pyela R., Ruegg C.;
RT "Characterization of human fibrinogen, a fibrinogen-like protein secreted by T lymphocytes."
RL J. Immunol. 161:1138-147(1998).
CC -1- FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT MUCOSAL SITES.
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC T-CELLS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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CC EMBL: Z65331, CA85298.1, -;
CC EMBL: AF104015, AADI0825.1, -;
CC EMBL: AF104014, AADI0825.1, JOINED.
CC HSSP: P02671; IP2D.
CC MIW: 605351; -;

```
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
KW T-cell; glycoprotein; signal.
FT SIGNAL 1 23
FT CHAIN 24 439
FT DOMAIN 210 435
FT DISULFID 213 242
FT DISULFID 371 384
FT CARBOHYD 25 25
FT CARBOHYD 179 179
FT CARBOHYD 235 235
FT CARBOHYD 263 263
FT CARBOHYD 336 336
SQ SEQUENCE 439 AA; 50228 MW; DF3465628BE49E68 CRC64;

Query Match 20.7%; Score 413.5; DB 1; Length 439;
Best Local Similarity 30.2%; Pred. No. 8,6e-26;
Matches 119; Conservative 61; Mismatches 147; Indels 67; Gaps 15;

QY 14 SSVNIIVEDGSNAKDESKNDTVCKEDCE-----ESCDVKTG 50
DQ 73 SRIEVEFKEVQNLKEIVSLKSKC-QDCKLQADNGDPERNGLLPSTGAPGEVGDNRVR 131
DQ 51 ITRKKHMKRCLONS---IYSTRSTKLLRN-----MDEQASLDIYSNOVNEIM 100
DQ 132 ELESVKNLSLSEKNAKEINLHRLKELNLVNNMNIENYDSKVANLTFVANSIDGKC 191
DQ 101 NRVLTLTEVFVKQDLPFRHPVQSHGL--DCTDKIDTIGSVTKRPSGLYIIHPGSSRP 158
DQ 192 SKC-----PSEQIQSRPVQ-HLIYKDCSDY---AIGKSSERYRTPDKKNS 237
QY 159 FEVMCDMDYRGSGVTVIQKRIDGIDFORLWCDYLDGFGDLGFEWLGKIKFYIVNQK 218
DQ 238 FEVYCDMETMGSGMTVLQARLDGSTNFTQMDYKAGFNLRRFPLGDKIHLTL--KS 295
QY 219 TSMFLVVALESDDPLAASVNFLEDETRFKMHLGYSNAGDAFGLKKEKNQNM 278
DQ 296 KEMIRIDLEDNGVELVALKDQFVYANLEKYLRLHVGNYNTAGDALR-FKKHYNHDK 354
QY 279 PESTDVDNDGCRPACLVNGQSVKSHLNKGTGMWFNFCGANLNG-IHHSGLKLTATG 337
DQ 355 FETPDKNDNRPSG-----NCG-LYSSGWFEDMCLSANLNGKYHOKYRGVRNG 404
QY 338 IQMGTW--TKNSPVKIKSVSKIRMTNP-YFK 368
DQ 405 IFWGTWPGVSEAHPGYKSSFEKAKMIRPKHFK 438

RESULT 2
FGL2_MOUSE STANDARD; PRT; 432 AA.
AC P12804;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast precursor (Fibrinogen-like protein 2) (Prothrombinase)
DE (Cytotoxic T-lymphocyte specific protein).
GN FGL2 OR FIBLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cytotoxic T-cell;
RX MEDLINE=87175527; PubMed=3550794;
RA Koyama T., Hall L.R., Hasegawa S., Saito H.;
RT "Structure of a cytotoxic T-lymphocyte-specific gene shows a strong
RT homology to fibrinogen beta and gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 84:1609-1613(1987).
```

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RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-BALB/CJ; TISSUE=Peritoneal macrophage;
RX MEDLINE=95333285; PubMed=7609073;
RA Parr R.L., Fung L., Reneker J., Myers-Mason N., Leibowitz J.L.,
RA Levy G.;
RT "Association of mouse fibrinogen-like protein with murine hepatitis
RT virus-induced prothrombinase activity.";
RL J. Virol. 69:5033-5038(1995).
CC -1- FUNCTION: CONVERTS PROTHROMBIN TO THROMBIN.
CC -1- SUBUNIT: HOMOTETRAMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC T-CELLS.
CC -1- INDUCTION: IN MACROPHAGES, DURING INFECTION BY MOUSE HEPATITIS
CC VIRUS STRAIN 3 (MHV-3).
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL: M16238; AAA57624.1; -.
DR EMBL: M15761; AAA37624.1; JOINED.
DR EMBL: S78773; AAA34823.1; -.
DR PIR: A27447; A27447.
DR HSSP: P02671; 1FZD.
DR MGD: MGI:103266; Fgl2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN-AG_C_DOMAIN; 1.
KW T-cell; Cytolysis; signal.
FT SIGNAL 1 19
FT CHAIN 20 432
FT DOMAIN 203 428
FT DISULFID 206 235
FT DISULFID 364 377
FT CARBOHYD 24 24
FT CARBOHYD 172 172
FT CARBOHYD 228 228
FT CARBOHYD 256 256
FT CARBOHYD 329 329
FT CONFLICT 332 332
SQ SEQUENCE 432 AA; 48951 MW; 2B297F69CBA4A782 CRC64;

Query Match 20.3%; Score 405.5; DB 1; Length 432;
Best Local Similarity 35.4%; Pred. No. 3,7e-25;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 78 LRMMMEQQA-----SLDIYSNOVNEIMNRVLLLTVEFRKQD-----PPR 119
DQ 137 LKNAKQIQLOGRLQLETLNLVNNMNIENYDNKVNAMLTVVV--NSLDGCKSCRPSQEHNQ 194
QY 120 HRVQSHGL--DCTDKIDTIGSVTKRPSGLYIIHPGSSVPEVMCDMDYRGSGMTVIQK 177
DQ 195 SQPVQ-HLIYKDCSD-HYVLG---RSSGAYRVTPRHRKSSFEVYCDMETMGSGMTVLQA 249
QY 178 RIDGIDFORLWCDYLDGFGDLGFEWLGKIKFYIVNQKNTSMFLVVALESDDPLAAY 237
DQ 250 RLDGSTNFTREWKDYKAGFNLRRFPLGDKIHLTL--KSKMIRIDLEDENGLTLYA 307
QY 238 STDNFWLEDETRFKMHLGRYSNAGDAFGLKKEKNQNMARSTSDVNDGCRPACLVN 297
DQ 308 LYDQFVANEFGKYLRLHIGNYNTAGDALR-PSRNHDLRFETPDNDNRPSG---- 362
QY 298 GQSVKCSHLNHNKGTGMWFNFCGANLNG-IHHSGLKLTATGIMGTWTKNN--SPVTKS 354
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DR EMBL; AF125176; AAD5358.1; -
DR HSSP; P02671; 1E2D.
DR MGD; MG1:1347003; Angptl2.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal; coiled coil; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 1 493 ANGIOPOIETIN-RELATED PROTEIN 2.
FT DOMAIN 77 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 202 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 57118 MW; 22885ABBE0746BF2 CACG64;

Query Match	20.0%;	Score 400.5;	DB 1;	Length 493;
Best Local Similarity	26.7%;	Pred. No. 1.1e-24;		
Matches 107; Conservative	66;	Mismatches 107;	Indels 121;	Gaps 15;

```

OY      48 KTKTRPEKHNMCSNLONSIVSYSTRSKKLLRYNMDDQASLDYLSNOVVELNNPVLLT 107
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      119 EVKLKRRES-----RNMMSRV-----TQLYMOLLHEITKRDNAL-----ELSDLEIRLLNOT 166
OY      108 TEVER-----KOLD-----PPRPPR-----122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      167 ADMJQLASKYKDEHKFOHJLAMLANQSEVIAOLEHCRQVRAPRMPQPRRPAAPRVYQ 226
OY      123 -----YQSH-----GJDSOTDKDITGSVTKPSC-----146
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      227 PRTYNRILINOISTNEISDONLKVLPRLPSTLRPALTSLPSTSTKPSGPMWDCLOALEDH 286
OY      147 -----LYIIRPESSYPREVMCDMDYREGGVTYIOKRIDGIIIDPORMLCBDYLDGFDLGE 202
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      287 STSYIYLKRENTNRKLNOQWCMDDORHDEGGMTVYIQRILDSGVNFRNNKETTQKQFGNIDGE 346
OY      203 FWLGLKKTIFYVNOKNTSEMLUYVLALESDDTLVAYSVDNFWLEDETRFFKMHILGRYSGNA 262
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      347 YWLGLEIYMWLTNGN--YKLTLYTMEBWSGRKVAEYASRLERPESEYUYLRIAGRYHGN 404
OY      263 GDAPFRGLKEDNOQNAPESTSVDYDNDGCRPACLNVGOSVYKSGSHLNKTKGWFNEBGLAN 322
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      405 GDSFTW-----HNGKOFITLLDRDHD-----YVTG-----NCAN-YOKGGMWYNACASHN 447
OY      323 LINGIHFSKGLLA---TGIDMGTMTKNNSPVKIKYSVMKTR 360
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      448 LINGWYIRGCHYRSRYODGYVADE--RGGSYSLKTKVMMIR 486

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RESULT	5			
ANL2_HUMAN				
ID	ANL2_HUMAN	STANDARD;	ERT;	493 AA.
AC	OSK9;			
DT	15-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Angiopolectin-related protein 2 precursor (Angiopolectin-like 2).			
GN	ANGPRL2 OR ARP2.			
OS	Homo sapiens (Human).			
OS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Heart;			
RX	MEDLINE:99403103; PubMed:10473614;			
RA	Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,			

RA	Koh G.-Y.	Molecular cloning, expression, and characterization of angiotensin-II-related protein. angiotensin-II-related protein induces endothelial cell sprouting."	RL J. Biol. Chem. 274:26523-26528(1999).	CC	-1- FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN AUTOCRINE AND PARACRINE ACTION.	CC	-1- SUBCELLULAR LOCATION: Secreted.	CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, SMALL INTESTINE, SPLEEN AND STOMACH. ALSO FOUND IN LOWER LEVELS IN COLON, OVARY, ADRENAL GLAND, SKELETAL MUSCLE AND IN PROSTATE.	CC	-1- PTM: N-GLYCOSYLATED.	CC	-1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.	CC	-----	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way CC modified and that this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcement/ or send an email to license@isb-sib.ch).	CC	-----	DR	EMBL; AF125175; AAD55357.1; -	DR	HSSP; P02671; 1PZD.	DR	MM; 605001; -	DR	InterPro: IPR002181; Fibrinogen_C.	DR	Pfam: PF00147; fibrinogen_C; 1.	DR	SMART: SM00186; FBG; 1	DR	PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.	KW	Signal; Coiled coil; Glycoprotein.	FT	SIGNAL	1	22	POTENTIAL.	FT	CHAIN	23	493	ANGIOPOIETIN-RELATED PROTEIN 2.	FT	DOMAIN	76	115	COILED COIL (POTENTIAL).	FT	DOMAIN	152	206	COILED COIL (POTENTIAL).	FT	DOMAIN	438	450	FIBRINOGEN C-TERMINAL.	FT	CARBOHYD	164	164	N-LINKED (GLCNAC. . .) (POTENTIAL).	FT	CARBOHYD	192	192	N-LINKED (GLCNAC. . .) (POTENTIAL).	QD	SEQUENCE	493 AA; 57104 MW; 062A0BC653D185CA CnC64;	
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Query Match	20.0%;	Score 400;	DB 1;	Length 493;
Best Local Similarity	31.9%;	Pred. NO. 1.2e-24;		
Matches 94;	Conservative 50;	Mismatches 93;	Indels 58;	Gaps 11;

[illegible]

RESULT	6
FGLI-HUMAN	
ID	STANDARD:
AC	Q08130; Q960M6; Q96KWE;
DT	01-MAR-2002 (Rel. 41, Created)
DT	01-MAR-2002 (Rel. 41, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Fibrinogen-like protein 1 precursor (Hepatocyte-derived fibrinogen

```

Query Match      19.9%:  Score 398;  DB 1;  Length 312;
Best Local Similarity 34.3%:  Pred. No. 9.7e-25;
Matches 111;  Conservative 44;  Mismatches 115;  Indels 54;  Gaps 12;

QY      67  IVSYRSTRKTKLLRNMMDDQASDLTSLNQNVLNMLNRVLLITTEVERKQ----- 114
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

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Db	4	VFSTILVTALLI---	MOREISALIEDCAEQBMRLAQRVLLERLRVQKQYKIKQLQLEBNV	60
Qy	115	--LDPEPHRPVQSHG----	LDCTDIKDTIGSVTKPISGLYIIHPBGSSYPREYCMDDY	167
Db	61	QFLDKGDENVIVIDGSKRQYADCSSEIFENDQYKL----	SGFYKIKPLQSPAEFSYVCDMS-	115
Qy	168	RGGGWYIYQKRIQSIIDFOKLMDYLDGFCDDL---	GFWMLGKIKIFYIVNQXNFSMLY	224
Db	116	DGGGWYIYQKRIQSIIDFOKLMDYLDGFCDDL---	GFWMLGKIKIFYIVNQXNFSMLY	224
Qy	225	VALSEEDTLIAYSYDNFWMLEDETRFKMHLGRYSGNADAFRLKKEDNO-----	NAMP	279
Db	174	IDLADFEKNSYQAYQKFKYKDEKNEYELNIGYSSTAGDSLQGNHNPYQWASHQKRM		233
Qy	280	FSTSDVDNDGCRPACLVNGOSVSKSHLNTKGMWNECGLANGLNHSFGSKLLA---	T	336
Db	234	FSTDRDHNDNEGNCAREDS-----	GMWNECGLANGLNHSFGSKLLA---	281
Qy	337	GIOMGTWTKNNSPKYIKSVSMKIR	360	
Db	282	GIVWYTW--HGWMYLSKSVYMKIR	303	
RESULT 7				
FTIBB_BOVIN	STANDARD:	PRT:	468 AA.	
AC	P02676;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].			
GN	FGF.			
OS	Bos taurus (Bovine).			
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
OC	Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae;			
OC	Bovidae; Bovinae: Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE OF 1-4.			
RA	Blomback B., Doolittle R.F.;			
RT	"The sequence of amino acids at the N-terminal end of bovine			
RT	fibrinopeptide B.";			
RL	Acta Chem. Scand. 17:1816-1819(1963).			
RN	[2]			
RP	SEQUENCE OF 5-21.			
RA	Stoquist J., Blomback B., Mallen P.;			
RT	"Amino acid sequence of bovine fibrinopeptides.";			
RL	Ark. Kemi 16:425-436(1960).			
RN	[3]			
RP	SEQUENCE OF 22-53.			
RX	MEDLINE=79164394; Pubmed=434821;			
RA	Martinielli R.A., Ingilis A.S., Rubira M.R., Hageman T.C.,			
RA	Hurrell J.G.R., Leach S.J., Scheraga H.A.;			
RT	"Amino acid sequences of portions of the alpha and beta chains of			
RT	bovine fibrinogen.";			
RL	Arch. Biochem. Biophys. 192:27-32(1979).			
RN	[4]			
RP	SEQUENCE OF 44-468 FROM N.A.			
RX	MEDLINE=81199473; Pubmed=6262803;			
RA	Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;			
RT	"Characterization of a cDNA clone coding for the beta chain of bovine			
RT	fibrinogen.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).			
CC	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT			
CC	POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET			
CC	AGGREGATION.			
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS			
CC	(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.			
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY			
CC	THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA			
CC	CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES			
CC	CONVERTIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS			
CC	CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE			

Query Match	19.8%	Score 395;	DB 1;	Length 498;
Best Local Similarity	27.0%;	Pred. No. 3e-24;		
Matches 116;	Conservative 66;	Mismatches 126;	Indels 122;	Gaps 16

RESULT	9			
AGPL_MOUSE		STANDARD;	PRT;	498 AA.
ID	AGPL_MOUSE			
AC	008538;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Angiopoletin-1 precursor (ANG-1).			
GN	ANGPT1 OR AGPT.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9713463; PubMed=8980223;			
RA	Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,			
RA	Ryan T.E., Bruno J., Radzilewski C., Malsompierre P.C.,			
RA	Tancopoulos G.D.;			
RT	"Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by			

FT		secretion-trap expression cloning.";
RL	Cell 87:1161-1169(1996).	
CC	-I- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS	
CC	TYROSIENE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL	
CC	PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A	
CC	CRITICAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE	
CC	ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD	
CC	VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE	
CC	HEART EARLY DEVELOPMENT.	
CC	-I- SUBCELLULAR LOCATION: Secreted.	
CC	-I- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS	
CC	FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE	
CC	ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN	
CC	IN THE MENSENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE	
CC	ASSOCIATION WITH ENDOTHELIAL CELLS.	
CC	-I- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.	
CC		
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CC	use by non-profit institutions as long as their content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-stb.ch/announce/	
CC	or send an email to license@isb-stb.ch)	
CC		
DR	EMBL; U083509; AAB50558.1; -. .	
DR	HSSP; P02671; IFEZD.	
DR	MCD; MG1:108448; AspI.	
DR	InterPro; IPR002181; Fibrinogen_C.	
DR	Pfam; PF00147; fibrinogen_C; 1.	
DR	SMART; SMO0186; FBG; 1.	
DR	PROSITE; PS00514; FTBRIN_AG_C_DOMAIN; 1.	
KM	Glycoprotein; Coiled coil; Signal.	
FT	SIGNAL	1
FT	CHAIN	19
FT	DOMAIN	20 498
FT	DOMAIN	81 119
FT	DOMAIN	153 261
FT	DOMAIN	284 498
FT	CARBOHD	92 92
FT	CARBOHD	122 122
FT	CARBOHD	154 154
FT	CARBOHD	243 243
FT	CAROHD	295 295
SO	SEQUENCE	498 AA; 57505 MW; 285B4DDEC260D800 CRC64;

[illegible]

QY 295 LVNGSVKSCSLHKNKTGWNECCGLANGLIHHS-----GKLLATGICMGWTNNSPV 350
DB 442 MLTG-----GWMFDACGSPNLNGMEFTAGQNHGKL--NGIKWHYF--KGPSY 484
QY 351 KIKSVSMKIR 360
DB 485 SLRSTTMIR 494
RESULT 10
AGP2_HUMAN
ID AGP2_HUMAN STANDARD: PRT: 496 AA.
AC 015123: Q9NRK7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; PubMed=9204896;
RA Madsenpierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziejewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.,
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RL Science 277:55-60(1997).
RN [2]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=umbilical vein endothelial cells;
RX MEDLINE=20309815; PubMed=10766762;
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.,
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2.";
RL J. Biol. Chem. 275:18550-18556(2000).
CC - FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC - SUBCELLULAR LOCATION: Secreted.
CC - ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC - SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@sdb-sdb.ch).
CC -----
CC EMBL: AF004327; AAB63190.1; -
CC EMBL: AF187858; AAF76526.1; -
CC HSSP: P02671; 1FZD.
CC MIM: 601922; -
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil; Signal; Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 496 ANGIOPOIETIN-2.

FT DOMAIN 130 256 COILED COIL (POTENTIAL).
FT 280 496 FIBRINOGEN C-TERMINAL.
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 97 148 MISSING (IN ISOFORM 2).
SQ SEQUENCE 496 AA; 56919 MW; 5642A58847A7385C CRC64;
Query Match 19.1%; Score 381.5; DB 1; Length 496;
Best Local Similarity 26.3%; Pred. No. 3.6e-23;
Matches 110; Conservative 73; Mismatches 138; Indels 97; Gaps 16;
QY 3 YGNCVCHHSDSSVNVIVDGSNANDESNQTVCKEDEDSCDVTKI-----TREE--- 55
DB 112 IQQNAVQNOT---AVMIDIGTLNLT-----AEQTRKLTDEAQLNQTTRLEQL 160
QY 56 -KHFMCRN-LQNSIVSYTRSTFKL-----LRNMDEQOASL 89
DB 161 LEHSLSTNKLKQILDQTSIKKLDQKNSFLKKVYAMEDKHIIQLQSIKEKQQLQVLY 220
QY 90 DYLSNOVNELMNRVLLT--TEVFRKQ-----LDPRPHRVOSH 126
DB 221 SKQNSIIELEKRIYATVYNNVSLQKQHDLMETVNNLTMTMSTNSAKDPYVAREQIS 280
QY 127 GIDCDIDIKTISVYKTPSPGLYIIHPEGSSYFEVWCDMDYGGGTVYQRIIDGIDRPQ 186
DB 281 FRDCAEVFKS-----GHTTGITVTLTPNSTEIKKAVCDMEAGGWTIIQREDDSVDRQ 336
QY 187 RLWCYLDGFGDLDGEFWLGLKRIEYVQKNTSFMLYVALESDDTLVASYDQNFMLED 246
DB 337 RHWKEKVGEGFNPSPGEYTWLGNFVSQLTNQQR--VYLKHLKLDWGENEAYSLXEHYLLSS 394
QY 247 ETRFFKMLHGRYSGNAGDAFRIGLKEDNONAMPFSTSDVNDGCRPACILVNGSVKSCSH 306
DB 395 EELNYRIHKLGLTPGAKI-----SSISQPGNDPSTKDGDDNCK-----ICKSQ 439
QY 307 LVNKGWMEFNECCGLANGLIH-----FSGKLLATGICMGWTNNSPVYKSVSMKIR 360
DB 440 MLT-GGWMFDACGSPNLNGMEFTAGQNHGKL--NGIKWHYF--KGSYSLAKATYTMIR 492
RESULT 11
FIBR_HUMAN
ID FIBR_HUMAN STANDARD: PRT: 491 AA.
AC P02675;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [contains: fibrinopeptide B].
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.,
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=83283433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.,
RT "Characterization of complementary deoxyribonucleic acid and genomic
RT deoxyribonucleic acid for the beta chain of human fibrinogen.";
RL Biochemistry 22:3244-3250(1983).
RN [3]

RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 fibrinogen.";
 RL (in) Liu C.Y., Chien S. (eds.);
 RL fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
 RL Plenum Press, New York (1991).
 RN [4]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (in) Peeters H. (eds.);
 RL Proteids of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [5]
 RP SEQUENCE OF 31-491.
 RX MEDLINE-79124640; PubMed-420779;
 RA Watt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:68-76(1979).
 RN [6]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE-76225080; PubMed-936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [7]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE-87146483; PubMed-3029722;
 RA Huber P., Dalmon J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RT beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 RN [8]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [9]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE-83254370; PubMed-6575689;
 RA Henschen A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE-77245999; PubMed-891553;
 RA Gaarlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RT disulfide-containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 RN [11]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Neurath H. (eds.);
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [12]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE-84305751; PubMed-6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE-97472408; PubMed-9333233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its

RT crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE-98292395; PubMed-9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-99175089; PubMed-10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [16]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE-89058942; PubMed-3194892;
 RA Schmelzer C.H., Ebert R.F., Bell M.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RT structural studies of fibrinogen Baltimore II.";
 RL Thromb. Res. 52:173-177(1988).
 RN [17]
 RP VARIANT ISE.
 RX MEDLINE-91208409; PubMed-2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the
 RT replacement of B beta glycine-15 by cysteine.";
 RL Blood 77:1958-1963(1991).
 RN [18]
 RP VARIANT NAPLES.
 RX MEDLINE-92340664; PubMed-1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta
 RT 68 Ala->Thr.";
 RL J. Clin. Invest. 90:238-244(1992).
 RN [19]
 RP VARIANTS JUMUIDEN AND NIMEGEN.
 RX MEDLINE-92228809; PubMed-1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens Jumuiden (B beta Arg14->Cys) and Nijmegen (B
 RT beta Arg44->Cys) form disulfide-linked fibrinogen-albumin
 RT complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [20]
 RP VARIANT NEW YORK-1.
 RX MEDLINE-85157605; PubMed-3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RT exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 CC -I- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -I- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -I- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC -I- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS

RT chain CDNA: interspecies conservation of fibrin beta 15-42 primary
 RT structure.";
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).
 RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RA MEDLINE=84194000; PubMed=6232608;
 RT Fowlkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
 RL "Potential basis for regulation of the coordinately expressed
 RT fibrinogen genes: homology in the 5' flanking regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RA MEDLINE=89378771; PubMed=2673932;
 RT Eastman E.M., Giulia N.B.;
 RL "Cloning and characterization of a cDNA for the B beta chain of rat
 RT fibrinogen: evolutionary conservation of translated and
 RT 3'-untranslated sequences.";
 RL Gene 79:151-158(1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.
 RC STRAIN-WISTAR; TISSUE=Liver;
 RX MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotli A.-M., Taroux P., Duguet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 RT liver regeneration.";
 RL Exp. Cell Res. 169:47-56(1987).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC -1- POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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 CC -----
 DR EMBL; U05675; AAA64866.1; -;
 DR EMBL; M27220; AAA41160.1; -;
 DR EMBL; K01336; AAA98625.1; -;
 DR EMBL; M35602; AAA41159.1; -;
 DR PIR; A05299; A05299;
 DR PIR; PE0010; PE0010;
 DR HSP; P02673; IFEZ;
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM Blood coagulation; Plasma; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
 FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
 FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
 FT DISULFID 219 304 (BY SIMILARITY).
 FT DISULFID 229 258 (BY SIMILARITY).
 FT DISULFID 412 425 (BY SIMILARITY).
 FT CARBOHD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
 FT CONFLICT 439 439 L -> Q (IN REF. 5).
 FT CONFLICT 441 441 S -> T (IN REF. 5).
 FT CONFLICT 445 445 S -> A (IN REF. 5).
 FT CONFLICT 467 467 R -> K (IN REF. 5).
 FT CONFLICT 475 475 V -> F (IN REF. 5).
 SQ SEQUENCE 479 AA; 54303 MW; EC6C6DB77C3E0E6C CAC64;
 Query Match 18.7%; Score 373.5; DB 1; Length 479;
 Best Local Similarity 27.2%; Pred. No. 1.5e-22;
 Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;
 QY 5 GNCVHSTDSVYNIVEDGSSNAKDSKSDIYCKEDCESCVKRTITREEHFRCRLQ 64
 DB 81 GGCYHDDGDMGL-----CATGCELRQTLNHE-----RPK 112
 QY 65 NSIV-----SYRSTKKILRMDEQASLDIYLSNONE----- 98
 DB 113 NSIAELNSINSVYETSTFQYLTLKDMKKKQAVQNDENVINEYSSILEDKLYTD 172
 QY 99 -----LMNVLTLTEVERKOLD-----PEFHRPVOSH-----GLDCTDI 133
 DB 173 ETVNDNIPRLNLRVLSILEDLSKMKKLESDISAQTEYCHPTVCYNCPVYSGKECEBI 232
 QY 134 KPTIGSVKTPSGLYIHPESSYYPEVWCMDYRGCGFTVYQKRIIDIFQRLMCDYL 193
 DB 233 IRKGGET-----SEMYLIQDTSKSPRYVCDMKTEGSGWTYIQRNODGSVDFGRKMDPYK 288
 QY 194 DGFGE-----LIGFELGLKRTFYVQKNSEFMVLYALESDDTLAVASYDN 241
 DB 289 KEGNATNEDTKKTCGLGELWLGNDKISQLTRIGPTE--LLIEMDKGDKVAHHGG 346
 QY 242 FWEDETRFEKMHILGRYSNAGDAF-----RGLKREDN-----ONAMPFSTDVNDGCRPA 293
 DB 347 FIVQTEANKYGVSVNKKYGTAGNALMEGASQLVGENRTWTHNGEFFSYDRDNDG---- 402
 QY 294 CLYNGSVASGCHLNKTKTWMEFEGLANLNGIHFSGL-----LATIQNGTWTK 345
 DB 403 -WYTTDPRRQCSK-EDGGGMWYNRCHAMPNGRYWGLYSWMSKHGTDGVVMWNV-- 458
 QY 346 NNSPVKIRKSKIRRMV 363
 DB 459 KGSWISMRMSKIRPVF 476
 RESULT 15
 FT FIBB_CHICK
 AC 002020; STANDARD; PRT; 463 AA.
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrinogen beta chain precursor [contains: Fibrinopeptide B]
 DE (Fragment).
 GN FGB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_Taxid=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
 RA MEDLINE=91182745; PubMed=2009266;
 RX Weissbach L., Oddoux C., Procyk R., Grlengier G.;
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin
 RT cleavage site.";
 RL Biochemistry 30:3290-3294(1991).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:08:30 ; Search time 29.86 Seconds
(without alignments)
1184.222 Million cell updates/sec

Title: US-09-596-196-9

Perfect score: 2000

Sequence: 1 EVVQGNCHVHSTDSVVNVIV.....PVKIKSVSMKIRMYNPK 368

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

- 1: PIR_71:*
- 2: PIR1:*
- 3: PIR3:*
- 4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	20.7	439	2	fibrinogen-like pr
2	405.5	20.3	432	2	cytotoxic T-lympho
3	401.5	20.1	432	2	fibrinogen-like pr
4	397	19.9	312	2	fibrinogen-related
5	394.5	19.7	468	1	fibrinogen beta ch
6	375.5	18.8	491	1	fibrinogen beta ch
7	371.5	18.6	437	1	fibrinogen gamma-A
8	371.5	18.6	453	1	fibrinogen gamma-B
9	371.5	18.5	463	2	fibrinogen beta ch
10	370	18.5	479	2	fibrinogen beta ch
11	365	18.2	444	2	fibrinogen gamma-B
12	360	18.0	432	1	fibrinogen gamma-B
13	352.5	17.6	438	2	fibrinogen gamma c
14	350.5	17.5	282	2	fibrinogen gamma c
15	348.5	17.4	774	2	scabrous locus (sc
16	346.5	17.3	328	2	fibrinogen beta ch
17	337.5	16.9	866	2	fibrinogen alpha c
18	330	16.5	1356	2	janusin precursor
19	329	16.4	334	2	fibrinogen alpha c
20	328.5	16.4	641	1	fibrinogen alpha-I
21	327.5	16.4	1353	1	transferrin precurs
22	312	15.6	437	1	fibrinogen gamma-A
23	311.5	15.6	445	1	fibrinogen gamma-B
24	311.5	15.6	445	1	tenascin-X bovin
25	310.5	15.5	1810	1	tenascin precursor
26	304.5	15.2	1914	2	tenascin Y precurs
27	303.5	15.2	326	2	ficolin-1 precursor
28	302.5	15.1	3566	1	tenascin-X precurs
29	302.5	15.1	440701	1	tenascin-X precurs

30	299	14.9	417	2	tenascin-X - pig (
31	296	14.8	220	2	tenascin homolog -
32	295	14.8	326	2	ficolin-beta - pig
33	286	14.3	860	2	tenascin-X - mouse
34	284.5	14.2	2019	1	tenascin precursor
35	283.5	14.2	4006	2	tenascin precursor
36	282.5	14.1	1746	1	tenascin precursor
37	271	13.6	2201	2	tenascin precursor
38	212.5	10.6	463	2	tenascin-C - human
39	180.5	9.0	915	2	hypothetical prote
40	180.5	9.0	927	2	hypothetical prote
41	173	8.7	431	2	hypothetical prote
42	154.5	7.7	933	2	cytoactin - chick
43	128.5	6.4	452	2	hypothetical prote
44	117	5.8	127	2	microfibril-associ
45	110.5	5.5	4588	2	dynein beta heavy

ALIGNMENTS

RESULT 1
fibrinogen-like protein expressed in T lymphocytes (pt49) - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I37391; S47273
R:Ruegg, C.; Pytel, R.
Gene 160, 257-262, 1995
A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib
A:Reference number: I37391; MUID:95369700
A:Accession: I37391
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-439 <RES>
A:Cross-references: EMBL:Z36531; NID:9535184; PID:CAA85298.1; PID:9535185
A:Note: submitted to the EMBL Data Library, August 1994
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	20.7%	Score 413.5;	DB 2;	Length 439;
Best Local Similarity	30.2%	Pred. No. 2.9e-25;		
Matches 119;	Conservative 61;	Mismatches 147;	Indels 67;	Gaps 15;
QY	14	SSVNIIVEDGSNADESKSNDTVCKE-----ESCQVYTK 50		
Db	73	SRIEEVFKEVONLKEIVNSLKKSC-QDCKIQADNDGDEGRNGLLPTSGAPGEVDNRVR 131		
QY	51	ITREKHFMCNLONS-----IVSYTRSTKILLRN-----MDQQAFLDLSNOVNEFLM 100		
Db	132	ELESEVNLISSELKAKKEIVNLHGRLEKLVNNNNIENYVDSKVAALTFVNSLDCKC 191		
QY	101	NRVLITTEVFRRKQDPPRRPVQSHGL-DCTDIKDTIGSVTFPPSGLYIIHPEGSSYP 158		
Db	192	SKC-----PSEQIQSRPVQ-HILYKDCSDV-----AIGRRSSFTYVTFDPPKSS 237		
QY	159	FEVCMQMDYRGQGWTVIOKRIDGIIDFORLWCDYLDGFDLLGEFGLKLIPIYVNOKN 218		
Db	238	FEVCDMETMGCGWTVLOARLDGSGTFNFRWQDKAGGNNRREFWLGNDKIHILT--KS 295		
QY	219	TSPMLYVALSEDDTLAAASYDNNFLDETRPFKWHIGRYSGNMGDAFRGLKKEDNQAM 278		
Db	296	KEMILRIDLEPNNGVELALYDQFVAEEFLKRLHVGNNYGTAGDALR-FNKHYNDLTK 354		
QY	279	PEFSTDVNDGCRPACTLVNGOSVKSCHLHNKGTGMWFECCGLANLG-IHFFSGKLLATG 337		
Db	355	FETTPDKNDNRYPSC-----NCG-LYYSSGMMFPACLSANLNGKYYHXKRGVANG 404		
QY	338	IQWGTW--TKNNSPVKIKSVSMKIRMYNP-YFK 368		
Db	405	IFWGTWPGVSEAHFGYKSSFEAKMIRPKHF 438		

RESULT 2

A27447
cytotoxic T-lymphocyte-specific protein precursor (clone p149) - mouse

C.Species: Mus musculus (house mouse)

C.Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999

C.Accession: A27447

R.Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Salto, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987

A.Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to

A.Reference number: A27447; MUID:87175527

A.Accession: A27447

A.Molecule type: mRNA

A.Residues: 1-432 <KOY>

A.Cross-references: GB:M16238; NID:g193304; PIDD:AAA37624.1; PTD:g387156

C.Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology <FBG>

i203-438/Domain: fibrinogen beta/gamma homology

Query Match	20.38;	Score 405.5;	DB 2;	Length 432;
Best Local Similarity	35.48;	Pred. No. 1.2e-24;		
Matches 110; Conservative	43;	Mismatches 115;	Indels 43;	Gaps 13;

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Oy 78 L R N M D E Q A ----- S L D Y S N Q N E L M N R V L L T T E F K R O L D ----- P P P 113
Db 137 L R N A K D Q I Q G L O G R L E T L I H L V N N N I E Y V D N K A V A N L T V V Y -- N S L D G K S C K P S O E H M O 194
Oy 120 H R P V O S H G L -- D C T D I K D I T G S V K T P S G L Y I I H P E G S S Y P F E Y C M D M Y R G G G W T V I O K 177
Db 195 S O P V Q - H L I Y K D C S D - H V L T L -- R R S S G A V R Y P D R H R N S S F E Y C C M E T M G S V T L A 249
Oy 178 R I D G I D E O R L A M C Y L O G S F G L D G E F M I G L K I P E Y I N O K N T S P M L V A L E S D P T L A Y A 237
Db 230 R I D G S T N T R E M K O Y K A G F G H L E R E F W I G N D K I H L T L -- K S K E I L R I D L E D F N G L T L Y A 307
Oy 238 S Y D N F W E D E T R F F R M H L G R Y S G N A G D A F R G L K E D N O N A M P S T S D V D N D G C R P A C L V N 297
Db 308 L Y D F E Y V A N E F L K R L H I G N T G N T A G A D A L R - F S R R Y N H D L R F F T T P R D R D R P S G --- 362
Oy 298 G O S V S C S C H L I N N K G M V N E C G L A N L I N G - I H H F S G C L L A T I G I O W G T W T K N N -- S P V K I S 354
Db 363 ----- N C G - L Y S S G W M F D S C L S A N L N G K Y I H Q K Y K G V R N G I E M G T V P G I N O A P G S Y K S 416
Oy 355 V S M K I R M Y N P 365
Db 417 S F K O A K M I R P 427

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RESULT      3
156934      fibrinogen-like protein - mouse
C:Species:  Mus sp. (mouse)
C:Date:      26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: 156934
R:Parr, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A:Title:      Association of mouse fibrinogen-like protein with murine hepatitis virus-induced
A:Reference number: 156934; MUID:95333285
A:Accession: 156934
A:Status:      Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues:    1-432 <RES>
A:Cross-references: GB:S78773; MID:g1042169; PIDN:AMB34823.1; PID:g1042170
C:Genetics:
A:Gene:      musfib1p
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-438/Domain: fibrinogen beta/gamma homology <FBG>

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Query Match	20.1%;	Score 401.5;	DB 2;	Length 432;
Best Local Similarity	35.0%;	Pred. No. 2.6e-24;		
Matches 109;	Conservative 43;	Mismatches 116;	Indels 43;	Gaps 13;

QY	78	L R N M M D E O A ----- S D Y L S N O V E L M N R V L L T T E V F R K O L D ----- P P P 119
Db	137	L K N A D Q I O G L O G R L E T L H L V N N N I E V Y D N K A N I L T V V - - N S L D K S C K S P S O E H M O 194
QY	120	H R P V O S H L - - D C D I K P T T S V M K T P S G L I I H R E S S Y P F E Y M C D M D R G G G V Y I O K 177
Db	195	S O P V O - H L I Y K D C S D - H Y V L G - - - R S S G A R V Y P D H R N S S F E Y U C M E T M G G V Y L Q A 249
QY	178	R I D G I I D F O R L M C D V L D S F G D L L E B F W M L G K I F Y I N O K T S P M L V A L E S E D D T L A V A 237
Db	250	R L D S T N T F R E M K O Y K A G F M L E R E F W L G N K I H L L - - K S E M I L R I D L E D R F G L T Y L A 307
QY	238	S Y D N F W L E D E T R F E K M I L G R Y S G N A G O A F R L G K E D N O M A P E S T S D V D N D G C R P A C V N 297
Db	308	L Y D Q Y V A N E F L K Y R L I G N Y N G S G O A L R - F S N H Y M H D L R F L T T P R D R D R P S G - - - 362
QY	298	G O S V A S C S H L N K T G W M F N E C G L A N L G - I H F S G K L L A T G I O M G V T K A N N - - S P V K I K S 354
Db	363	----- N C G - L Y U S S O M W D C S L A N L G K Y H Q Y K G V R N G I I F W G T V P G I N O A O P G G Y K S 416
QY	355	V S M K I R R M Y N P 365
Db	417	S E K O A K M I R P 427

```

RESULT 4
JN0596
fibrinogen-related protein HFREP-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
R:Yamamoto, T.; Gottoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related
A:Reference number: JN0596; MUID:93290661
A:Accession: JN0596
A:Molecule type: mRNA
A:Residues: 1-312 <YAM>
A:Cross-references: GB:D14446; NID:g393314; PIDN:BA00336.1; PID:g393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HFREP-1 #status predicted <MAT>
E:80-305/Domain: fibrinogen beta/gamma homology <FBS>

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Query Match	19.9%	Score 397	DB 2	Length 312
Best Local Similarity	34.3%	Pred. No. 3.9e-24		
Matches 111	Conservative 44	Mismatches 115	Indels 54	Gaps 12
QY 67	IVSYRSTKLLRNMMDEQASIDLYLSNQNVLNMLNVLITLTFVEPRKO-----	114		
DB 4	VSFILVITLAL---MGREISALEDCAOEMIRRAVRLLETRVKQOQVKKIQLLOENEV	60		
QY 115	--LDPEPRHVPYOSH-----LDCTDIKIDTIGSVYTKTSPGLVYIIHPGSSYPPEVMCDMDY	167		
DB 61	QFLDKKDEDEDTVVDLSGRQYADOCSELFNNGYKL-----SGFYKIKPLQSPAEFSVYCDMS-	115		
QY 168	RGGWTVIOKRIDGIIIDFORLMCDYIDGEGDLL--GEFWLGIKLTFTYLVNOKNFSMLY	224		
DB 116	DGGWTVIOKRISGSENFGRGWKDYENGNGFNFFVQKIGHEVLEGNKMLNHLFTTQED--YTLK	173		
QY 225	VLESSEDDTFLVASYDNFMLEDETFREKHLNLRYSGNACDARGLCKEENO-----NAMP	279		
DB 174	IDLDAFEKSRRAQYKNEFVVGDEKNFYELNIGETYSCTAADSILAGNPNHPEVQWMASSIQRMK	233		
QY 280	FSTSDVNDGCRPACPLVNOQSVKSCSHLNTKGTWMEFNEGCLANLNGIHHFSKLLA--T	336		
DB 234	FSTWDRDHDTNYNGNCAQEDGS-----GWMNRRCHSANLNGV--YSGGYTAKTDN	281		
QY 337	GIONGTWTRKNSBPVKTIKSVSKIR	360		
DB 282	GIVWYTW--HGWWYSILKSVVMKIR	303		

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RESULT 5
FGHOB
fibrinogen beta chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Jul-1981 #sequence-revision 29-Jul-1981 #text-change 13-Sep-1996
C:Accession: A03122; B03117; B37507; A37513; S02443
C:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A03122
A:Accession: A03122
A:Molecule type: protein
A:Residues: 1-4 <BLO>
R:Sjoquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A:Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: protein
A:Residues: 5-21 <SJO>
R:Martinehl, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrinopeptides.
A:Reference number: A37507; MUID:79104394
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen.
A:Reference number: A37513; MUID:81199473
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Luknova, N.I.
FEBS Lett. 232, 56-60, 1988
A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; MUID:88211875
A:Accession: S02443
A:Molecule type: protein
A:Residues: 373-374 <MED>
C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide B.
C:Superfamily: fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide C; Keywords: blood coagulation; glycoprotein; plasma; pyroglyutamic acid; sulfoprotein F; 76-205/Domain: fibrinogen disulfide ring homology <PDR>
F; 215-464/Domain: fibrinogen beta/gamma homology <FBG>
F; 1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F; 6/Binding site: sulfate (Tyr) (covalent) #status experimental
F; 21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F; 371/Binding site: carboxylate (Asn) (covalent) #status predicted
F; 372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 19.7%; Score 394.5; DB 1; Length 468;
Best Local Similarity 27.3%; Pred. No. 1e-23;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;

Oy 7 CVHSTDSVYNIEDSNKDESKSNDYCKEDCESDVKTKITREKHF--MCNQLQ 64
Db 72 CLHADPPLGLV-----CPYCKKIOTDLVAKOERPIKRSIEDLR 108

Oy 65 NSIVSYRSTRK-----LIRNMMDQOASLDYLSNOVNLMM----- 101
Db 109 NTVDSVSRSTSSFTQYITLKKNMKGNQONQONENYVNESSLSLEKHQYIDFTVKNNI 168

Oy 102 -----RVLLITTEVFRKQDLDFP-----HRPVQSHGLDCTDIKDTIGS 139
Db 169 PTKLRVLRSLIEILNRKIKOKLESVDSTOMEXCRTPCTVTGNIPIVVS--GKECEKILIRNEGE 227

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RESULT 6
FGHUB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence-revision 31-Mar-1993 #text-change 08-Dec-2000
C:Accession: B43568; A90469; B90469; I37389; A94433; A94309; G54223; A03121;
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; MUID:91344740
A:Accession: B43568
A:Molecule type: DNA
A:Residues: 9-191, 'P', 193-491 <CHU>
R:Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A:Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyrib
A:Reference number: A90469; MUID:83283433
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CHU>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191, 'A', 193-491 <CH2>
A:Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R:Huber, P.; Dalmont, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A:Title: Characterization of the 5'-flanking region for the human fibrinogen beta gen
A:Reference number: I37389; MUID:87146483
A:Accession: I37389
A:Molecule type: protein
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R:Henschen, A.; Lotspeich, F.; Southan, C.; Topfer-Petersen, E.
In: Protides of the Biological Fluids, Proc. 28th Colloq., Petersen, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
A:Reference number: A94433
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137, 'OS', 140-144, 'OF', 147-491 <HEN>
R:Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; MUID:79124640
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144, 'OF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976

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A:Residues: 27-437 <HEN>
 R.Kant, J.A.; Lord, S.T.; Crabtree, G.R.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
 A:Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: ex
 A:Reference number: A93956; MUID:83247396
 A:Accession: B93956
 A:Molecule type: mRNA
 A:Residues: 276-437 <KAN>
 R.Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
 J. Biol. Chem. 259, 12826-12830, 1984
 A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
 A:Reference number: A92448; MUID:85030379
 A:Accession: B92448
 A:Molecule type: DNA
 A:Residues: 286-437 <FOR>
 R.iman, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
 Nucleic Acids Res. 11, 7427-7434, 1983
 A:Title: Isolation and characterisation of cDNA clones for the Alpha- and gamma-chains
 A:Reference number: 137393; MUID:84069777
 A:Accession: 137393
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 209-270 <RES>
 A:Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:9577055
 R.Bertagnoli, M.E.; Beckerle, M.C.
 J. Cell Biol. 121, 1329-1342, 1993
 A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th
 A:Reference number: A40696; MUID:93286185
 A:Accession: A40696
 A:Molecule type: protein
 A:Residues: 27-33,'XX',36-41 <BER>
 A:Experimental source: thrombin-activated platelets
 R.Kunitake, S.T.; Carilli, C.T.; Lau, K.; Procter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
 A:Reference number: A54223; MUID:94162201
 A:Accession: H54223
 A:Molecule type: protein
 A:Residues: 27-33,'XX',36-41 <KUN>
 A:Note: Identification of tryptic peptides from high-density lipoproteins
 R.Henschen, A.; Lotspelsch, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A:Title: Covalent structure of fibrinogen.
 A:Reference number: A90037; MUID:83254370
 A:Contents: annotation: review; disulfide bonds
 R.Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrill, B.A.; Cassman, K.G.; G
 In Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
 A:Title: The structures of fibrinogen and fibrin.
 A:Reference number: A94437
 A:Contents: annotation: disulfide bonds
 R.Blomback, B.; Hessel, B.; Hoger, D.
 Thromb. Res. 8, 639-656, 1976
 A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A:Reference number: A94309; MUID:83231465
 A:Contents: annotation: disulfide bonds
 R.Hoepflich, P.D.; Doolittle, R.F.
 Biochemistry 22, 2049-2055, 1983
 A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds
 A:Reference number: A90467; MUID:83231465
 A:Contents: annotation: quaternary structure, disulfide bonds
 R.Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A:Title: Fibrinogen and fibrin.
 A:Reference number: A90041; MUID:84305751
 A:Contents: annotation: review, EM structure, polymerization, ligands
 R.Horvitz, B.H.; Varadi, A.; Scheraga, H.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
 A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
 A:Reference number: A94006; MUID:85014892
 A:Contents: annotation: polymerization region
 R.Kloczewlak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
 Biochemistry 23, 1767-1774, 1984

A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and struct
 A:Reference number: A90483; MUID:44203545
 A:Contents: annotation: platelet aggregation region
 R.Plow, E.F.; Stoufi, A.B.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.
 J. Biol. Chem. 259, 5388-5391, 1984
 A:Title: Evidence that three adhesive proteins interact with a common recognition sit
 A:Reference number: A92477; MUID:84185664
 A:Contents: annotation: platelet aggregation region
 R.Dang, C.V.; Ebert, R.F.; Bell, W.R.
 J. Biol. Chem. 260, 9713-9719, 1985
 A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit posi
 A:Reference number: A92549; MUID:85261382
 A:Contents: annotation: calcium binding region
 R.Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH
 A:Reference number: A37117; MUID:90337977
 A:Contents: annotation: hematin cleavage site
 A:Note: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle
 A:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stab
 ger) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesized in the liver.
 C:Comment: The two forms of gamma chain, A and B (see PIR:FGHGB), arise by alternate
 intron, which makes this chain different from the gamma-B chain at positions 434-437
 C:Genetics:
 A:Gene: GDB:FGG
 A:Cross-references: GDB:119132; OMIM:134850
 A:Map position: 4q28-4q28
 A:Introns: 26/3: 41/3: 103/3: 134/2: 178/1: 222/3: 284/2: 377/1: 433/3
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR
 ins are contained in the core. Two three-chain coiled coils emerge from this core and
 from the distal domain nodes.
 C:Function:
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
 A:Pathway: blood coagulation
 C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-437/Product: fibrinogen gamma-A chain #status experimental <MPN>
 F:176-415/Domain: fibrinogen beta/gamma homology <BGB>
 F:341-355/Domain: calcium binding #status predicted <CAB>
 F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
 F:423-437/Region: platelet aggregation #status predicted
 F:34/Disulfide bonds: Interchain (to gamma-35) #status experimental
 F:35/Disulfide bonds: Interchain (to gamma-34) #status experimental
 F:45/Disulfide bonds: Interchain (to beta-110) #status experimental
 F:49/Disulfide bonds: Interchain (to alpha-64) #status experimental
 F:78/Binding site: carbohydrate (asn) (covalent) #status experimental
 F:161/Disulfide bonds: Interchain (to beta-227) #status experimental
 F:165/Disulfide bonds: Interchain (to alpha-180) #status experimental
 F:179-208, 352-365/Disulfide bonds: #status experimental
 F:424/Cross-link: isopeptide (Gln) (Interchain to Lys-432 N6-amino) #status experimen
 F:432/Cross-link: isopeptide (Lys) (Interchain to Gln-424) #status experimental

Query Match 18.68; Score 371.5; DB 1; Length 437;
 Best Local Similarity 31.9%; Pred. No. 6.5e-22;
 Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

QY 65 NSIYSYRSTKRLRNMDQ-----QASIDYLSNQNVELMNRVLLTTEVFRQDLPF 118
 DB 103 NMIDAATLKSRKMLEIKTPEASITTHDSITRYLOEIVSNNNQKIVNKEKV--AQLEAO 160
 QY 119 PHRP-----GLDCTDIDKDTGSVTRTPSGILYIHPEGSSYPPEWCMDDYRGGG 171
 DB 161 CQPECKDVTQVQHDITGKRCQD-----IANKGAKOSGLYTRKPLKNAQOFLYVCEIDGSGNG 216
 QY 172 WTVYQKRIDGIIIDPQRLWCYDLDFGDI-----LGEFWLGLKKIFYIVNQKTSFMYVAL 227
 DB 217 WTVFQKRIDGSDVPEKKNMIVQYKGFHLSPTGTETFWLGNKRIHLISFOAIPYALRVEL 276

```

QY 228 ESEDDTLAVASYDNFWLEDETRFRFEMHLGRYS-GNAGDAFRGLKKE-----NONAM 278
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EDWNGRTSTADYAMFKYGPEDADKRLTYAYFAGDGADAFGDFGDDPSDKFTFSHNM 336
QY 279 PESTSDVNDGCRPACLVNAGOSVSCSHLHNKTKGWFMNECGLANINGIHHSFGKL----- 333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 QESTWINDNDKFRGNCABQDGS-----GWMNKKCHAGHLNGVYVGQGVYSKAST 385
QY 334 ---LATGIOMGTWTKNNSPVKIKSVSMKI 359
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 PNGYDNGIIMATW--KTRWYSMKTKTKMI 412

RESULT 8
FGHUGB
N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C>Date: 17-Mar-1987 #sequence-revision 17-Mar-1987 #text-change 08-Dec-2000
C:Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1-113,'1',115-453 <RIX>
A:Cross-references: GB:M10014; GB:J00134; GB:X00086; NID:9182438; PIDN:AA595
R:Forname Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <FOR>
R:Mofenstien-Todol, C.; Mosesson, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxyl-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Reference number: A90453; MUID:82068993
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <WOL>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A:Reference number: A94194; MUID:88217900
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 433-453 <FR2>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334
A:Accession: I37390
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 75-286 <RES>
A:Cross-references: EMBL:X51473; NID:931410; PIDN:CA53837.1; PID:9930064
C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate spli
nition, which makes this chain different from the gamma-B chain at positions 434-437 and
C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas
C:Genetics:
A:Gene: GDB:FGG
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Initons: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
lins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C:Function:

```

```

A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-453/Product: fibrinogen gamma-B chain #status experimental <MPT>
F:341-355/Domain: fibrinogen beta/gamma homology <FRG>
F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-110) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted
F:78/Binding site: carbonyl (Asn) (covalent) #status predicted
F:161/Disulfide bonds: interchain (to beta-227) #status predicted
F:165/Disulfide bonds: interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

```

Query Match 18.6% Score 371.5; DB 1; Length 453;

Best Local Similarity 31.9% Pred. No. 6.8e-22; Mismatches 129; Indels 53; Gaps 11;

Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

```

QY 65 NSIVSYSTRKLLRNMQD-----QASLDLSNQVLMNRYLLTTEVFRKQDPF 118
      | : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 NMIDATLTKSRKMLEIMKYEASILTHDSSIRLYDEIVSNNOKVLYNKEKY--NOLEAQ 160
QY 119 PRRP-----QOSH---GLDSTDIKDTGTSVTKRPSGLYIINHPGSSYPRFVMDMDVRGG 171
      | : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 COEPCKDTQVYHDITGKCDQD---IANKAKOSGLYFKPKLAKANOQFLVCEIDSSGNG 216
QY 172 WTVIQKRIDGIIDFQRLMCDYLDGFGLD---LGEFMLGLKRIFYLVNOKTSMFYVAL 227
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 WTVFQKRIDGSVDFPKKNWQYKGFEGHLSPTGTTEWLCNEKHILHSQALRYALRYVL 276
QY 228 ESEDDTLAVASYDNFWLEDETRFRFEMHLGRYS-GNAGDAFRGLKKE-----NONAM 278
      | : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EDWNGRTSTADYAMFKYGPEDADKRLTYAYFAGDGADAFGDFGDDPSDKFTFSHNM 336
QY 279 PESTSDVNDGCRPACLVNAGOSVSCSHLHNKTKGWFMNECGLANINGIHHSFGKL----- 333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 QESTWINDNDKFRGNCABQDGS-----GWMNKKCHAGHLNGVYVGQGVYSKAST 385
QY 334 ---LATGIOMGTWTKNNSPVKIKSVSMKI 359
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 PNGYDNGIIMATW--KTRWYSMKTKTKMI 412

RESULT 9
fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 31-Jul-1991 #sequence-revision 31-Jul-1991 #text-change 13-Aug-1999
C:Accession: A38463
R:Weissbach, L.; Oddoux, C.; Procyk, R.; Grlengier, G.
Biochemistry 30, 3290-3294, 1991
A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745
A:Accession: A38463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <MEI>
A:Cross-references: GB:M58514; NID:9211779; PIDN:AAA48770.1; PID:9211780
F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FRG>

```

Query Match 18.6% Score 371.5; DB 2; Length 463;

Best Local Similarity 27.7% Pred. No. 7e-22; Mismatches 136; Indels 99; Gaps 17;

Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;

QY 25 NAKDESKNDYVEDCE-----ESCDAVKTKITREEKHMCRLNLSYSTRS 73
1 30 NSEBMASSNDNTKONVOTI DPT NSPSSCHVMAOK FTENDYKFKVTP -TSTVAGCI PS 188

[illegible]

RESULT 12
fibrinogen gamma chain precursor - sea lamprey
C:Species: Petromyzon marinus (sea lamprey)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 20-Oct-2000
C:Accession: A03129
R:Strong, D.D.; Moore, M.; Cottrell, B.A.; Bohonus, V.L.; Pontes, M.; Evans, B.; Riley, B.
Biochemistry 24, 92-101, 1985
A:Title: Lamprey fibrinogen gamma chain: cloning, cDNA sequencing, and general character
A:Reference number: A03129; MUID:85199776
A:Accession: A03129
A:Molecule type: mRNA
A:Residues: 1-432 <STR>
A:Cross-references: GB:K03049; NID:9213193; PID:AAA49262.1; PID:9213194
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation; glycoprotein; liver; plasma; pyroglyutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-432/Product: fibrinogen gamma chain #status experimental <MP>
F:15-411/Domain: fibrinogen beta/gamma homology <FBG>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim
F:227/Binding site: carboxylate (asn) (covalent) #status predicted
F:421/Cross-link: isopeptide (Gln) (interchain to Lys-425 N6-amino) #status predicted
F:425/Cross-link: isopeptide (Lys) (interchain to Gln-421) #status predicted

Query Match 18.0%; Score 360; DB 1; Length 432;
Best Local Similarity 30.1%; Pred. No. 5.3e-21;
Matches 115; Conservative 52; Mismatches 151; Indels 64; Gaps 16;

QY 13 DSSVNIYEDGNSNADE-SKSDNYCKEDCESCDYKTKITEKHEKRNQNSIVST 71
DB 62 DSSFDISVLTQLAARHGIVEGNVNIIVNE-VRITRDEAQIIDSQKTYOKIL 113
QY 72 RSTKRLNNMDEQASLDYLS-NO-VNELRNRYLLTTEVFRKQDPPFRPVQ 124
DB 114 EEV-RILQIGVSHDAQOELSEMKRVNQFVTRIQOQLVDVROTCRSCQDTANKIS 172
QY 125 SHGLDCTDIKDTIGSVTKPSGLYIHPGSSYPFVCMDDYRGSGWTVIQKRIDGI 184
DB 173 ITGKCCQGVNDGK-DSGLYIKPLKAKQPLVCEIE-NGNGWTVIOHRHDSVN 227
QY 185 FORLMCDYLDGFG-DLGEFNLGKIKFIYVQKNTSFMLYALAEEDDTLAYASD 240
DB 228 FTRDWSYRSEFGYLAPTLTTEFWLGNKRIHLLTGOO-AVRLRIDLDWMENTHRYADG 285
QY 241 NFWL--EDETR-PEKMLHGRYSNAGDAFRGLKKEDNON-----AMPSTSDVD 288
DB 286 HFKLPREDEYRLFTSMTL--DGDAGNAFDGDFGDDPQDKFYTHGLMLFSTPERND 342
QY 289 GCRPACLVNGQSVKCSHLHNKTGWMFNECGLANLNGIHFSGLLAT-----GIOW 340
DB 343 KYEGSCAQDGS-----GWMNMRCHAGHLNGKYYFGNRYKRTDVEFPYDDGIIM 391
QY 341 GMTKNNSPVKIKSVSMKIRRM 362
DB 392 ATW-HDRWYSLKMTTKLPLM 411

RESULT 13
A32670
fibrinogen gamma chain - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
C:Accession: A32670; I51416
R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
Biochemistry 29, 2599-2605, 1990
A:Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
A:Reference number: A32670; MUID:90241882
A:Accession: A32670
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-438 <PAS>
A:Cross-references: GB:J02894; NID:9214139; PID:AAA49709.1; PID:9214140
R:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
Mol. Cell. Endocrinol. 72, 213-220, 1990
A:Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenop
A:Reference number: I51416; MUID:91146806
A:Accession: I51416
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-58 <BHA>
A:Cross-references: GB:M35548; NID:9214141; PID:AAA03247.1; PID:9214142
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: blood coagulation
F:173-413/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.6%; Score 352.5; DB 2; Length 438;
Best Local Similarity 27.2%; Pred. No. 2.1e-20;
Matches 106; Conservative 54; Mismatches 141; Indels 89; Gaps 14;

QY 39 EDCESCDYKTKITREKHF--MCRNLQNSIVSTRSKLLRNMD-----EQQ 86
DB 41 EVCPTGIGISDFLNRYQENVDFDQYLENLQINSSTGTTIIVHLLIDSGKKPATSPQ 100
QY 87 ASD-----YISQVNELMNRVLLTTEVFRKQD-FF 118
DB 101 TAIPTOKSKTCMKLTDKNYYQENILYLQEVYSSNQNKIFLLKOKIANLELQCOQ 160
QY 119 PHRPV-----QSHGLDCTDIKDTIGSVTKPSGLYIHPGSSYPFVCMDDYRGSGWT 174
DB 161 PCRDYVOIDFETKDCQEVANKGARL-----SGLYIKPLKAKQPLVCEIEPSSGSAWTV 216
QY 175 IOKRIDIIDFORLMCDYLDGFGDL--LGEFNLGKIKFIYVQKNTSFMLYALAESE 230
DB 217 IORLDGSVNFHKNQVYREGFYLSPNDKTEFNLGNKRIHLLTQSTIPRYVRIELOW 276
QY 231 DDTLAYASDNPFL--EDETR-PEKMLHGRYSNAGDAFRGLKKD-----NQNM 278
DB 277 SNOKSTADYSTFRLGSEKQNYRFTYAVFTG--GDAGADFDFGDDPDKFTYTHNG 333
QY 279 PESTSDVDNDGCRPACLVNGQSVKCSHLHNKTGWMFNECGLANLNGIHFSGLT----- 333
DB 334 QPSTFPKDNKDFGNCABEDGS-----GWMNMRCHAHNLNGKTYQGSGTYSEADS 382
QY 334 ---LATGIQWGTWTKNNSPVKIKSVSMKI 359
DB 383 GPSGYDNGIIMATWRRR--WYSKSVTKMI 410

RESULT 14
A35084
fibrinogen-related protein A precursor - sea cucumber (Parastichopus parvimeus)
C:Species: Parastichopus parvimeus
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Sep-1997
C:Accession: A35084
R:Xu, X.; Doolittle, R.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 2097-2101, 1990
A:Title: Presence of a vertebrate fibrinogen-like sequence in an echinoderm.
A:Reference number: A35084; MUID:90192754
A:Accession: A35084
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-282 <XUX>
A:Cross-references: GB:M31326; NID:9161164; PID:9161165
C:Superfamily: fibrinogen beta/gamma homology
F:67-280/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.5%; Score 350.5; DB 2; Length 282;
Best Local Similarity 36.8%; Pred. No. 1.8e-20;
Matches 92; Conservative 31; Mismatches 96; Indels 31; Gaps 10;

QY 113 KQDLPFRHPVQSHGLDCTDIKDTIGSVTKPSGLYIHPGSSYPFVCMDDYRGSGW 172

```
Db 58 KRISHPSPY-----RDYDYLQSC-SGQSPSPSGOYIYQPGGNC-IVYCOMMEIDEGM 110
Qy 173 TVIQRKIDGIDTIDFORLWCDYLDGEGDLDGFWLGLKFIYVYNQNTSPMLVVALESEDD 232
Db 111 TVFORRIDGIDTINFYKSMYSYOTGFGNLTWFERMLGNDNIHYLSQGD--YELFVEIINTLG 168
Qy 233 TLAVASYNFMLEDETREFKMLHGRYSGNAGDAPFRGLKKEEDNQNMPESTSDVDNDCGRP 292
Db 169 NHYIAKINKEFRIGDSFSEYLLVLGAYSGTAGDSL-----YHNTREFSTYDNDND---- 218
Qy 293 ACLVNGOSVSKCSH-LHNKTCGMFNECGLANLNGIH-FSGKLLATGIQWGTWTKNNSPV 350
Db 219 -----VISINCASHSSYRGAMWYKSCLSLNGOYIDYSG---APSIYWSLTPGDND-- 268
Qy 351 KIKSVSMKIR 360
Db 269 QIPFEMKLR 278
```

```
RESULT 15
A39832
scabrous locus (sca) protein precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 01-Dec-2000
C/Accession: A39832; S58998
R/Baker, N.E.; Mlodzik, M.; Rubin, G.M.
Science 250, 1370-1377, 1990
A/Title: Spacing differentiation in the developing Drosophila eye: a fibrinogen-related
A/Reference number: A39832; MUID:91075223
A/Accession: A39832
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-774 <BAK>
A/Cross-references: GB:M60065; GB:M37703; NID:g158401; PID:g158402
R/Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A/Title: Molecular analysis of scabrous mutant alleles from Drosophila melanogaster indi
A/Reference number: S58998; MUID:96109607
A/Accession: S58998
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-18, 'T', 20-774 <HUX>
C/Genetics:
A/Gene: FlyBase:sca
A/Cross-references: FlyBase:FBgn0003326
C/Superfamily: fibrinogen beta/gamma homology
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>
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```
Query Match 17.4%: Score 348.5; DB 2; Length 774;
Best Local Similarity 25.1%: Pred. No. 9.2e-20;
Matches 100; Conservative 65; Mismatches 137; Indels 97; Gaps 14;
```

```
Qy 14 SSVAVIVEDGNSNAKDESKNDPTVCKEDCEESCDVTKIT-----REEKHFCRNLONSI 67
Db 360 TSMLELEDVDEGLQTKMKKSIPELRHEISKLEFFANAQITSEOSLIREBGTNARSILQAMA 419
Qy 68 VSYT-----RSTKRLRNMDQDQASLDYLSNOVNEIMNRYL----- 104
Db 420 VSVSVLQEREGMKRLSAN-VDQLRTNVDRLOSLVNDKMKNLTLNKPVRKHRRHQNQA 478
Qy 105 -----LITTEV-----FRKQDPPRHPRVOSHGLDCTDIKDTIGSVTKT 143
Db 479 QMPDDSPIDSVLAETLVSELENVETOYEAIINKLPH-----DCSEVH-----TOT 524
Qy 144 PSGLYIHPEGSSYPFEVNCMDYRGGMVYQKRIDGIDFORLWCDYLDGFGDLGEF 203
Db 525 -DGLHLIAPACORHRLMHTCAD-----GWTYQRRFDGSADPNRSMADYAGFGAGGEF 579
Qy 204 WLGLKIFIVYNQNTSPMLVVALESEDDTLAVASYDNFMLEDETREFKMLHGRYSGNAG 263
Db 580 WIGNQQLHHLT--LDNCSRLQGVOMODIYDNVAVAEYKRFYISSRADGYRLHIAEYSGNAS 637
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Qy 264 DAFRGLKKEEDNQNMPESTSDVDNDCGRPACLVNGOSVSKCSHLHNKTCGMFNECGLANL 323
Db 638 DAL-----NYOQMGQFSAIDDDRDISIOTHCAANEFG-----GMWFSHCQHANL 680
Qy 324 NCIIHFSGLKLTATGIQWGTWTKNNSPVKIKSVSMKIRRM 362
Db 681 NGRYNL-----GLTWPDARNEW-IAVSSRLMLVKRL 711
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Search completed: May 22, 2002, 15:08:31
Job time: 198 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:07:54 ; Search time 22.62 Seconds
(without alignments)
397.375 Million cell updates/sec

Title: US-09-596-196-9

Sequence: 1 EVYQNCVCHHTDSSVNVIV.....PVKIKSVSMKIRMYNPFYK 368

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2.6/prodata/2/1aa/5a_COMB.pep:*
2: /cgn2.6/prodata/2/1aa/6a_COMB.pep:*
3: /cgn2.6/prodata/2/1aa/6a_COMB.pep:*
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5: /cgn2.6/prodata/2/1aa/6b_COMB.pep:*
6: /cgn2.6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	21.2	491	2	US-08-933-821-4
2	425	21.2	491	3	US-08-960-507-4
3	425	21.2	491	4	US-09-136-828-4
4	405.5	20.3	490	4	US-08-740-223A-12
5	403.5	20.2	487	4	US-08-740-223A-4
6	402.5	20.1	487	1	US-08-373-579-4
7	402.5	20.1	487	2	US-08-418-595-4
8	402.5	20.1	487	2	US-08-665-926-4
9	402.5	20.1	487	2	US-08-348-492-4
10	402.5	20.1	487	4	US-09-162-437-4
11	400	20.0	483	2	US-08-933-821-2
12	400	20.0	483	3	US-08-960-507-2
13	400	20.0	483	4	US-09-136-828-2
14	399	19.9	482	1	US-08-525-505A-4
15	395.5	19.8	486	4	US-08-740-223A-22
16	395	19.8	478	4	US-08-740-223A-7
17	395	19.8	485	4	US-08-740-223A-26
18	395	19.8	486	4	US-08-740-223A-2
19	395	19.8	488	4	US-09-351-457-2
20	395	19.8	488	4	US-09-561-500-2
21	395	19.8	488	4	US-09-561-108-2
22	394	19.7	485	4	US-09-351-457-5
23	394	19.7	485	4	US-09-561-500-5
24	394	19.7	485	4	US-09-561-108-5
25	393	19.6	491	4	US-08-740-223A-13
26	389	19.4	314	1	US-08-525-505A-2
27	389	19.4	498	1	US-08-373-579-2

28	389	19.4	498	2	US-08-418-595-2	Sequence 2, Appl
29	389	19.4	498	2	US-08-665-926-2	Sequence 2, Appl
30	389	19.4	498	2	US-08-348-492-2	Sequence 2, Appl
31	389	19.4	498	4	US-09-162-437-2	Sequence 2, Appl
32	387.5	19.4	497	4	US-08-740-223A-14	Sequence 14, Appl
33	381.5	19.1	480	4	US-08-740-223A-8	Sequence 8, Appl
34	381.5	19.1	486	1	US-08-373-579-6	Sequence 6, Appl
35	381.5	19.1	486	2	US-08-418-595-6	Sequence 6, Appl
36	381.5	19.1	486	2	US-08-665-926-6	Sequence 6, Appl
37	381.5	19.1	486	4	US-09-162-437-6	Sequence 6, Appl
38	381.5	19.1	486	4	US-08-740-223A-6	Sequence 6, Appl
39	381.5	19.1	486	4	US-09-351-457-4	Sequence 4, Appl
40	381.5	19.1	486	4	US-09-561-500-4	Sequence 4, Appl
41	381.5	19.1	486	4	US-09-561-108-4	Sequence 4, Appl
42	381.5	19.1	489	4	US-08-740-223A-24	Sequence 24, Appl
43	381	19.1	498	4	US-08-740-223A-20	Sequence 20, Appl
44	379.5	19.0	346	3	US-08-960-507-19	Sequence 19, Appl
45	375.5	18.8	491	1	US-08-206-176-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-08-933-821-4
; Sequence 4, Application US/08933821
; Patent No. 5972338
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: The Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 491 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-933-821-4

Query Match 21.2% Score 425; DB 2; Length 491;
Best Local Similarity 26.9%; Pred. No. 2.5e-37;
Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

Oy 24 SNADDESDNDFVKECESDVYKTKITRE-EKHFMCRNIONSVYSTRKTLNNMM 82
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 68 TKGDASTIKMTIRMDLENKIDVLSRKREIDVLOLVVDGNVIVKILRRESNMN 127
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Oy 83 DE-QQASIDVY-----SNQVNEIMNRVLLITTE----- 109
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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Db	128	SRVQLVQLLHEIIRKRDNSLETQLENKILNTVTEMLKATRYRELEVKASLTDLVN	167
QY	110	-----VERKQ-----LDP-----FPHRPVQSHGL-----	128Q
Db	188	NQSWMITLLEEQCLRIIRSDTHVSPPLVQVPPHNIENSOOYTPGLGLGNEIORDPYPR	247Q
QY	129	DCDTIKDPIGSEVTKP-----SGLTIIHEGSSPYFEV	161Q
Db	248	DLMPPLDIAVTSKSPKIPRPYVIFINSGPRKCOQAKGASHVSGLYIMIPENSNGMQL	307Q
QY	162	MCDMDYRGCGWTVYQKRIKIDGIIDEFQRLMCDYLDGFGDILGEFVLGKKIPIYVNOKRTSF	221Q
Db	308	WCENSLDPGGWTVYQKRTDGSVNFERNMMENTKKGFNGIIDEYEWGLGLENITMLSNQDN--Y	365Q
QY	222	MLYVALESEDDTLAYASIDNFWLEDETFREFKMLGRYSNAGDAFRGLKREDONAMFPS	291Q
Db	366	KLILELEWDSMKKYVAEYSSFRLEPESEEFRLRIGTQYGNACGSMW-----HNGKQFI	419Q
QY	282	TSDVDNDCGRACLVNQSVASCSCHLINTKQGWPMNEGGLANLNGCIHHFSKLLA-----TGI	338Q
Db	420	TLDDDKD-----MYAGNCNHFH--KGGWVYNACAAHSNLNGVWYRGGHYRSKHODGI	468Q
QY	339	QMGTVTKNNSPVKIKSVSMKIR	360Q
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RESULT 62
 US-08-960-507-4
 Sequence 4, Application US/08960307
 Patent No. 6057435
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinpatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/960,507
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130p1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 491 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-960-507-4

	Query Match	21.2%	Score 425;	DB 3;	Length 491;
	Best Local Similarity	26.9%	Pred. No. 2.5e-37;		
	Matches 119; Conservative	64;	Mismatches 133;	Indels 126;	Gaps 14.
OY	24	SNADESKSNIVYCKEDCECDVTKITRE-EKHFMCNLSNSTVSYRSTRKKLLRNMM	82		
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Db      68  TKGQDASTIKDMITRMDELNKDVLRSQKREIDVLQLVVDGNIYEVKLKESNNM 127
QY      83  DE-QQASIDYL-----SNQVNEIMNRVLLITL-----109
Db      128  SRVTLQYMLLHEIIRKRDNLSELEENKILNVTTEMLMATRYRELEVKYASLTDLVN 187
QY      110  -----VFRKQ--LDP-----FHRPVQSHGL-----128
Db      188  NOSVMTLLEEQCLRIKRSRODTHVSPFLVQVVRPHIIPNSOQYTPGLLGGNEIORDQYPR 247
QY      129  DCTDIKDTIGSVTKP-----SGLYIHPESSYFVEY 161
Db      248  DLMPPPLDIAETPTKSPKIPVPTFINGEPFKDCQAKKASHSVSGIYKIPENSNGPML 307
QY      162  MCDMDYRGGGTIVLOKRIIDGIIIDQRLMCOYLDSFGDGLLEFMYGLKRIYIYNQKNTSF 221
Db      308  WCESNSLDPRGWTIVLOKRTDGSVNEFRMWEENTKKGFNGIDGYMLGENTIMYLSNODN--Y 365
QY      222  MLYVALESEDDTLLVASYADNFWLEDETRFRFKMILGRYSGNAGCAFLRGLKKEDQNAMPFS 281
Db      366  KLILELEDMWSKKYYAEKSSRLREBESEFRLRLRGTYIQGNAGDSMMK-----HNCKQFI 419
QY      282  TSDVDNDCRPACLVNGOSVSKSCHLHNKTKGMWFNECCGLANLNGIHHSCKLLA---TGI 338
Db      420  TLDRDKD-----MYAGNCNHFH-KGGWVWYNAACASHNLGCVWYRGCHYRSKHDQGI 468
QY      339  QMGTWTKNNSPVKIKTSVSMKR 360
Db      469  FWAELY--RGGSYSLRAVQNMIR 488

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3
 US-09-136-828-4
 Sequence 4, Application US/09136828
 Patent No. 6350450
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: Tle Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minipatln (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136, 828
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130R1A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 491 amino acids
 TYPE: Amino acid
 TOPOLOGY: Linear
 US-09-136-828-4

Query Match	21.28;	Score 425;	DB 4;	Length 491;
Best Local Similarity	26.98;	Pred. NO. 2.5e-37;		

	Matches	119;	Conservative	64;	Mismatches	133;	Indels	126;	Gaps	14
Qy	24	SNAREBSKSNIPVCKEEDCEESCDVYKTIKRE-EKHMKCNLONISYSTRSTYKLLRNMA	82							
Db	68	TKGQASITKIDMITKMDLENKLDVYSRQKREIDVQLVYDVGNINVEYKLLRKESRRNN	127							
Qy	83	DE-QQASIDYL-----SNQVELMKRVLLTTE-----	109							
Db	128	SNVQLVYQGLHLEIKRKRNDSLELSQLEKKILNVTTEMLKMATRYRELEVKVASLTDLVN	187							
Qy	110	-----VFKQ--LID-----FPHRPVOSHGL-----	128							
Db	188	NQSVMITLLEECLEIFFSKODTHVSPRLVQVPHNIPNSOQYTPGLLGNETIQRDGYPR	247							
Qy	129	DCTDIKDTIGVSTKRP-----SGLYIHPEGSSYPFEV	161							
Db	248	DLMPRPDLATSTKSPKFRPYTFPIFNEGPFKQCOAKKEGHSVSGTYMKPKPENSNPML	307							
Qy	162	MCDMDYRGSGWTVIQKRIDGITDFORLWCDYLDGFGDILGFWLGLKTFUYIVNOKNTSF	221							
Db	308	WCENSLDRCGWTVIQKRTGDSVNFEEFMWENYKKGFENINGEGWLGLENITMLSNOQN--Y	365							
Qy	222	MLYVLESBDTFLAASYNFWLEDETRFKFNHLGYSQNAQDAFGLKKEDQNAMPSS	281							
Db	366	KLILEEDMSDKKVAEYSSFRLEPSESEYRIALGLYQSNAGOSMMW-----HNGKQFL	419							
Qy	282	TSVDVNDGCRPACLVNGQSVKSCSHLNNHTGWMFNECGLANLNGIHHFSGLKLA---TG	338							
Db	420	TLDPRKD-----MYAGNCANFN-KGGMWYNACASHSNLNGVYRGHNYRSKHQDGI	468							
Qy	339	QMGVTWKNNSPYKIKSVSKIR	360							
Db	469	FMAEY--RCGSYSLRAVQMMIK	488							

RESULT 4
 US-08-740-223A-12
 Sequence 12, Application US/08740223A
 Patent No. 6263564
 GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed ligand - Vascular
 TITLE OF INVENTION: Intercellular Signalling Molecule
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill Road
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/740.223A
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 60/022/999
 FILING DATE: 02-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Cobert, Robert J
 REGISTRATION NUMBER: 36,108
 REFERENCE/DOCKET NUMBER: REG 333
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEFAX: 914-345-7721
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids

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?      TYPE: amino acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
?      FEATURE:
?      NAME/KEY: hTTL1
?      LOCATION: 1...490
?      OTHER INFORMATION: human TIE-2 ligand 1
?      US-08-740-223A-12

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Query Match	20.3%;	Score 405.5;	DB 4;	Length 490;
Best Local Similarity	27.5%;	Pred. No. 3.3e-35;		
Matches 118;	Conservative 65;	Mismatches 125;	Indels 121;	Gaps 16;

OY	3	VQGNCHNSTDSVYNIVEDGSNNKDESKSNDTJCKEDCESJCQVTKTRIPREKHFMCRN	62
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OY	63	LONSTVS------TSTKKLLRNMM	82
Dd	157	LENSITJKLEKOLLQOTNEILKTHEKNLSLEHKILEMEGKHKEELDTLKEEKENLOGLV	216
OY	83	DEQASLDLYSNQN------ELM-----NRVLLTFEVF-----RKQDDPR	119
Dd	217	TROYUUIOELEKOLRRATTNNSVLOKOOLEIMDTVMNLVNLCJEVLLKSGKREEKRPF-	275
OY	120	HBPVOHSGLDFTDKIDTGTSYTKTPSGUYIHHPGSSYPFEVMCDMDYRGGWIVIOKRI	179
Dd	276	-----ROCADY------QAGFKMSGIYTIYINMPERPKKVPFCMBDVNGGWIVIOHRE	322
OY	180	DGDIIDFOYLKCDYLDGFSDLLGEFWMLGLKATFFIYNOKNSFMYLVALLESDDTLAYSY	233
Dd	324	DGSDIFOGMEYKXKMGFGFNPGSEYWLWLNDFEIFFATTSOR--OYMRLIELMEGNGRAVSQY	381
OY	240	DNFMLEDTEFRFKMHILGYSSNAGDAFRLKEDN--ONAMPFSTVDNDGCRRPAC--TL	295
Dd	382	DRFHIGNKQYVRXLXKGHTAG-----KQSSLIHGADFSBTDKADNDNCMKCALM	436
OY	296	VNGOSVKSCSHLHNKTGMWFNECGLANINGIHFS---GKLATGTGIOWCTWTAKNSPVK	351
Dd	435	LTG-----GWMFPDACPSNINCMGFYTAGONHGKL--NGIKWHYF--KGPSYS	477
OY	352	IKSVSMKIR	360
Dd	478	IRSTTMIR	486

RESULT 5
 US-08-740-223A-4
 ; Sequence 4, Application US/08740223A
 ; Patent No. 6265564
 ; GENERAL INFORMATION:
 APPLICANT: Davis, et al.
 TITLE OF INVENTION: Expressed Ligand - Vascular
 TITLE OF INVENTION: Intracellular Signalling Molecule
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 STREET: 777 Old Saw Mill Road .
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/740,223A
 FILING DATE: 25-OCT-1996
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Human TIE-2 ligand 1
LOCATION: 1...2146
OTHER INFORMATION: from T986 clone
US-08-740-223A-4

Query Match 20.2%; Score 403.5; DB 4; Length 497;

Best Local Similarity 27.3%; Pred. No. 5.5e-35;

Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQGNVHSTSDSVNIVIEDGSNARDESKNDTYCKEDCEESCDYKTKITREKHFMCRN 62
DB 115 IQQNAVQNHNT---ATMEIGTSLSQT-----AEQTRKLTVEQVLNQTSLREQL 163
QY 63 LQNSTIVSY-----ELM-----TRSTKLLRNMM 82
DB 164 LENSISTYKLEKOLLQOTNEILKIEHKNLSLEHKLMEGKHKEELDTLKEKENLQGLV 223
QY 83 DEQQAISLYLSNOVN-----NRYLLLTTEVF-----RKOLDPRP 119
DB 224 TRQYITIOLEKQLRATNNNSVLOKOLELMDYVHNLVNLTCTKEVLLKGGKREDEKPF- 282
QY 120 HRPVQSHGLDCTDIKDTIGSVTKTPSPGLYIIHPGSSYFPEVYCDMDYRGCGWTVIQKRI 179
DB 283 -----RDCAADV-----QAGFNKSGIYTYIYINMPPEKVKVFCMDVNGGWTYIQHRE 330
QY 180 DGIIDFQRLKCDYLDGFDLLGEFWLGLKTFIYVNOKNTSMLYVLALESDDTLAVASY 239
DB 331 DGSIDFQGWKWEYKMGFNPSPGSEYVLGNEFFAITSQR--QYMLRIELMDWEGNRAVASYQ 388
QY 240 DNFWLEDETRPFKMHILGRYSNAGDAFRGLKEDN--QNAMPFSTSDVNDGCRPAC--L 295
DB 389 DRFHIGNEKQNTRLYLKHTGTAG-----KQSSLILHGADFTSKDADNDNCMKCKCALM 441
QY 296 VNGQSVKSCSHLNKTKGWMFNECGLANLNGIHNFSG---KLLATGTGLOWGTWTKNNSPVK 351
DB 442 LTG-----GWMFADACPSNLNMGMYTAGQNHKRL--NGIKWHYF--KGPSYS 484
QY 352 IKSYSKAKIR 360
DB 485 LRSTTMIR 493

RESULT 6
US-08-373-579-4

; Sequence 4, Application US/08373579

; Patent No. 5650490

; GENERAL INFORMATION:

; APPLICANT: Davis, et al.

; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; RESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-373-579-4

Query Match 20.1%; Score 402.5; DB 1; Length 497;

Best Local Similarity 27.3%; Pred. No. 7.1e-35;

Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQGNVHSTSDSVNIVIEDGSNARDESKNDTYCKEDCEESCDYKTKITREKHFMCRN 62
DB 115 IQQNAVQNHNT---ATMEIGTSLSQT-----AEQTRKLTVEQVLNQTSLREQL 163
QY 63 LQNSTIVSY-----ELM-----TRSTKLLRNMM 82
DB 164 LENSISTYKLEKOLLQOTNEILKIEHKNLSLEHKLMEGKHKEELDTLKEKENLQGLV 223
QY 83 DEQQAISLYLSNOVN-----NRYLLLTTEVF-----RKOLDPRP 119
DB 224 TRQYITIOLEKQLRATNNNSVLOKOLELMDYVHNLVNLTCTKEVLLKGGKREDEKPF- 282
QY 120 HRPVQSHGLDCTDIKDTIGSVTKTPSPGLYIIHPGSSYFPEVYCDMDYRGCGWTVIQKRI 179
DB 283 -----RDCAADV-----QAGFNKSGIYTYIYINMPPEKVKVFCMDVNGGWTYIQHRE 330
QY 180 DGIIDFQRLKCDYLDGFDLLGEFWLGLKTFIYVNOKNTSMLYVLALESDDTLAVASY 239
DB 331 DGSIDFQGWKWEYKMGFNPSPGSEYVLGNEFFAITSQR--QYMLRIELMDWEGNRAVASYQ 388
QY 240 DNFWLEDETRPFKMHILGRYSNAGDAFRGLKEDN--QNAMPFSTSDVNDGCRPAC--L 295
DB 389 DRFHIGNEKQNTRLYLKHTGTAG-----KQSSLILHGADFTSKDADNDNCMKCKCALM 441
QY 296 VNGQSVKSCSHLNKTKGWMFNECGLANLNGIHNFSG---KLLATGTGLOWGTWTKNNSPVK 351
DB 442 LTG-----GWMFADACPSNLNMGMYTAGQNHKRL--NGIKWHYF--KGPSYS 484

QY 352 IKSVMKIR 360
Db 485 LRSTTMIR 493

RESULT 7

US-08-418-595-4
: Sequence 4, Application US/08418595
: Patent No. 5814464
: GENERAL INFORMATION:
: APPLICANT: Daviss, et al.
: TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/418,595
: FILING DATE: 06-APR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/373,579
: FILING DATE: 17-JAN-1995
: APPLICATION NUMBER: US 08/353,503
: FILING DATE: 09-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/348,492
: FILING DATE: 02-DEC-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/330,261
: FILING DATE: 27-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/319,932
: FILING DATE: 07-OCT-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Cobert, Robert J.
: REGISTRATION NUMBER: 36,108
: REFERENCE/DOCKET NUMBER: REG 330-D
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 345-7400
: TELEFAX: (914) 345-7721
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 497 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-418-595-4

Query Match 20.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 7.1e-35;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNCVHSTDSVVNIVEDSGSNADSKSNDTYCKEDCESDVKRTITREKHFMCN 62
Db 115 IQQNAVQNHNT---ATMEIGFTSLSQT-----AEQTRKLTIVETQVLTQTSRLTQL 163
QY 63 LQNSIVST-----TRSTKILRRMM 82
Db 164 LENSISTYLERKQLLOQTNETILKIEKNSLLEHKLILEMGKHKEBLDTLKEKENLQGLV 223

QY 83 DEQOASLDYLSNOVN-----ELM-----NRLLLTTEVF-----RKQDPFP 119
Db 224 TRQYIIOLELKRQUNRATNNNSVLQKQLELMDYVHNLVNLCTKEVLLKGKREEDRF- 282
QY 120 HRPVQSHGLDCTDIKDTIGSVTKTPPSGLYIHPGSSYPFEVWCMDMDYRGSGWTVIOKRI 179
Db 283 -----RDCADYV-----QAGFNKSGIYTYIYNMPEPKKVFPCNMVDVNGSGWTVIOHRE 330
QY 180 DGIIDFQRLKCDYLDGPFEDLGEFVLGKRTFYLYNOKNTSFMLYVALESDDTLATASY 239
Db 331 DGSIDPFGWKVEYKMGFGNPSGEYWLGNFTFATISQ- -OYMLRIELMDWEGNRAVSQY 388
QY 240 DNFMLEDTRPFKMHILGRYSGNAGDAFRLGKEDN- -ONAMPFSTPDVNDGCRPAC- -L 295
Db 389 DRFHIGNKQYRLYLKHTGTAG- -KQSLIHGADFSTKPDADNDNCCKCALM 441
QY 296 VNGOSVKSCHLHNKGTWFMFNECGLANLNGIHFS- -GKLTATGLOMGTWTRNNSPVK 351
Db 442 LTG-----GWWFADCGPSNLNGMEYTAGQNHKRL- -NGIKWHYF- -KGPSYS 484
QY 352 IKSVMKIR 360
Db 485 LRSTTMIR 493

RESULT 8

US-08-665-926-4
: Sequence 4, Application US/08665926
: Patent No. 5851797
: GENERAL INFORMATION:
: APPLICANT: Valenzuela et al.
: TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10591-6707
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/665,926
: FILING DATE: 19-JUN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Robert J. Cobert
: REGISTRATION NUMBER: 36,108
: REFERENCE/DOCKET NUMBER: REG 330-H
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 345-7400
: TELEFAX: (914) 345-2113
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 497 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-665-926-4

Query Match 20.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 7.1e-35;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

QY 3 VQNCVHSTDSVVNIVEDSGSNADSKSNDTYCKEDCESDVKRTITREKHFMCN 62
Db 115 IQQNAVQNHNT---ATMEIGFTSLSQT-----AEQTRKLTIVETQVLTQTSRLTQL 163

[illegible]

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: MOLECULE TYPE: protein
: US-08-348-492-4

Query Match 20.1%; Score 402.5; DB 2; Length 497;
Best Local Similarity 27.3%; Pred. No. 7.1e-35;
Matches 117; Conservative 66; Indels 121; Gaps 16.

QY 3 VQNCVHHSTDSVYVIVDGSNADESKSNDYVCKEDCEESCDYKTKITREKHPCRN 62
Db 115 IQQNAVQNT-----ATMEIGTSLSQ-----AEQTKLTVDYQVLYNTSRLQID 163
QY 63 LQNSIVSY-----TRSTKKLLRNMM 82
Db 164 LENSSTYKLEKQLLOQTNEILIKHEKNSLEKILEMEGKHKEBLDTLKEKENLOGLV 223
QY 83 DEQQAQLDYLSQNV-----ELM-----NRVLLLTTEVF-----RKOLDPP 119
Db 224 TQQTYYIDLEKQLNRATTNNSVLOKQOLEMDYVNLVNLCTKEYLLKGKREDEKPF- 282
QY 120 HRPVOSHGLDCTDIDKDTIGSVTKTPSGLYIIPRESSYFPEVCMDDYRGKGVYIOKRI 179
Db 283 -----RDCAVY-----QAGFNKSGIYITIIYINMPEKKVKECMDDYVGGMVYIOHRE 330
QY 180 DQIIDFQRLACMYDLOGFGLDGEFLLGKRTIYVYNQKTSFMLYVALESDDTLAYASY 239
Db 331 DQSLDFQRMKYEYKMGFGNPSGEYVWGNFGEIFALTSQR--QYMLREIEMDWMGNRAYSOY 388
QY 240 DNPWLEDFRPFKMHILGRYSGNAGDAFRGLKKEDN--QAMPEFSTDVYDNCRCRAP--L 295
Db 389 DPFHIGENQNRRLYLKGTHTAG-----KQSSLILHGADFSTKRDADNDCMKCALM 441
QY 296 VNGQSVKSCSHLHNTGMWFNECGLANLNGIHFS---GKLLATGIONGVTKNNSPVK 351
Db 442 LIG-----GMWFDAQSPSNLGMFYTAGQNHGKL--NGIKWHYF--KGPSYS 484
QY 352 IKSVMKIR 360
Db 485 LKSTTMIR 493

RESULT 10
US-09-162-437-4
: Sequence 4, Application US/09162437
: Patent No. 6166185
: GENERAL INFORMATION:
: APPLICANT: Davis, et al.
: TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Regeneron Pharmaceuticals, Inc.
: STREET: 777 Old Saw Mill River Road
: CITY: Tarrytown
: STATE: New York
: COUNTRY: USA
: ZIP: 10591
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/162,437
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/418,595
: FILING DATE: 06-APR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/373,579
: FILING DATE: 17-JAN-1995
: APPLICATION NUMBER: US 08/353,503

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FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
TELEFAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-162-437-4

Query Match 20.1%; Score 402.5; DB 4; Length 497;
Best Local Similarity 27.3%; Pred. No. 7.1e-35;
Matches 117; Conservative 66; Mismatches 125; Indels 121; Gaps 16;

3 VQGCVHHSTGSSVNVNIEDGSSNAKDESKSNDYJCKEDCESCVKPTITREKHFMCRN 62
115 IQQNAVQNHNT---ATMLEIGTSLLSQT-----AEOTKRLTIVEYOVNLQTSRLQL 163
63 LQNSIVSY-----TRSTKLLRNMM 82
164 LENSLSYFKLEKQQLQOETNELIKTHEKNSLLENHILEMEGKHEDLTLYKREKENLQGLV 223
83 DEQASLDYLSNOYV-----ELM-----NRVLLTTEVF-----RQOLDFP 119
224 TRQYTIIOELERKQNRATTTNSVLQKQQLMDTVHNLVNLCTKEVLLKGGKREEDKPF- 282
120 HRPVQSHGLDCTDIKDTIGSVTKTPSGLYIHPREGSSYFPEVMDCMYRGSGMTVYQKRI 179
283 -----RQCADYV-----QAGFNKSGIYTYIYINMPEPKVYFCMDYVNGSGMTVYQIRE 330
180 DGIIDFQRLMCDYLDGFGDLDGEFWLGLKLTLYVNOKNTSFMLYVALESEDDTLAVASY 239
331 DGSIDFGWKEYKMGKGNPSGEYWLGNFIFAITSQR--QYMLRIELMDWEGNRAYSQY 388
240 DNFULEDETREFKMHLDGRYSGNADAFRLKKEDN--QNAMPFSTSDVDNDGCRPAC--L 295
389 DRFHIGNKQYRILYLGHTGTAG-----KQSSLLIHGADFSTKDDNDNCKCKCALM 441
296 VNGOSVSKSHLHKTKGWFNECGLANLGIHFS---GKLLATGIQMGTWTKNNSPVK 351
442 LTG-----GWMFDACGSPNLNGMFTYAGQNHGKL--NGIKMHIF--KGPSYS 484
352 IKSYSVMKIR 360
485 LRSTTMMIR 493

RESULT 11
US-08-933-821-2
Sequence 2, Application US/08933821
Patent No. 5972338
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,821
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-933-821-2

Query Match 20.0%; Score 400; DB 2; Length 493;
Best Local Similarity 31.9%; Pred. No. 1.3e-34;
Matches 94; Conservative 50; Mismatches 93; Indels 58; Gaps 11;

97 NELMNRVLLTTEVFRKO-----LDPEPRVQSHGLDCTDIKDTIGSVTKTPSG----- 146
221 NRINQL--STNEIQSDQNLKVLPRPLPTMPLT-----SLPSTQKPSGPMWDC 278
147 -----LYIHREGSSYFPEVMDCMYRGSGMTVYQKRI DGIIDFQRLMCDYLD 194
279 LQALEDHGDTSSIVLYKKEENTRLMQVWCDOHRPGGCTVYQRRLDGSGVNFPRMMEYKQ 338
195 GFGDLDGEFWGLKKEIFLYVNOKNTSFMLYVALESEDDTLAVASYDNLWLEDETREFKMH 254
339 GFGNIDGTYWLGLENTIYTLNQG--YKLVYTMEDWSRKVFAETASRLPESESYTYLR 396
255 LGRYSGNAGDAFRGLKKEDNQAMPFSTSDVDNDGCRPACLVNGQSVKSHLHKTKGWM 314
397 LGRVHGNAGDSFTW-----HNGKQFTLLDRDHD-----VYTG---NCAH-YKGGWM 439
315 FNEGGLANLNGIHFSGKLLA---TGLOWGTWTKNNSPVKIKSYSMKIRRMATNY 366
440 YNACASHNLNGWVRGHYRSRYQDGYVMAEF--RGGSYSLKVVYMMIRPNPNTF 492

RESULT 12
US-08-960-507-2
Sequence 2, Application US/08960507
Patent No. 6057435
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4587-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-525-505A-4

Query Match 19.9%; Score 399; DB 1; Length 312;
Best Local Similarity 34.3%; Pred. No. 8.1e-35;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 67 IVSTSTKRLKLNMDQASLDYLSNQVNEIMNRYLLITTEVERKQ-----114
DB 4 VFSFIIVTTAL--MGREISALEDCAQEQMRLAQVRLLETRVKQCOQVRIKOLLQENEV 60
QY 115 --LDPPHRRPVQSHG-----LDCTDIKDTIGSVTKRPSGLYIIHPRESSYFVEVCMQMDY 167
DB 61 QPLDKGDENTVDLGSKROYADCESEIFNDGKYL---SGEYKIKPLOSPEFSSYCCMS- 115
QY 168 RGGGWTVIQKRIDGIDFORLWCDYLDGFGDL--GEFVLGLKIFIVYNOKNTSFMLY 224
DB 116 DGGGWTVIQGRSDGSENFNGWKDYENFGNFKHGEYWLGNKNLHFLTQED--YTLK 173
QY 225 VALESDDTLAVSYDNFMLEDETRFKMHLGRYSNAGDAFRGLKEDNO-----NAMP 279
DB 174 IDLADFEKNSRYAQYKFKKVGDEKNEFELNIGESGTAGCSLAGNFRPEVQWMAASHORMK 233
QY 280 FSTSDVNDGCRPACLVNQGOSKCSHLHNKTMWNECGLANLGIHPSGKLLA---T 336
DB 234 FSTWDRHDHVEGNCALQEDS-----GWFNRCNSANLNGV-YISGPTAKTND 281
QY 337 GIQMGTVTKNNSPYKIKSVSMKIR 360
DB 282 GIWYTW--HGWMYSLKSVMKIR 303

RESULT 15
US-08-740-223A-22
Sequence 22, Application US/08740223A
Patent No. 6265564
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: InterCellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill Road
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999

FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coberl, Robert J.
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: 2N2C1F (chimera 2)
LOCATION: 1...496
OTHER INFORMATION:
US-08-740-223A-22

Query Match 19.8%; Score 395.5; DB 4; Length 496;
Best Local Similarity 27.5%; Pred. No. 4.1e-34;
Matches 116; Conservative 68; Mismatches 133; Indels 105; Gaps 17;

QY 3 VQNCVHHSTDSVYNIIVEDGNSNAKDESKSNDYCKEDCEBSCDVTKI---TREE---55
DB 112 IQQNAVONQ---AVMIEIGTNLNTQ-----ABQTRKLTVDYEAQVNLQTRLEQL 160
QY 56 -KHFMCRN-LQNSIVSYTRSTKRL-----LRNMDQASL 89
DB 161 LEHSLSTNKLKQILDQTSSEINKLQDKNSLEKVLAMEDKHITQLOSIEEKQDLQVL 220
QY 90 DYLSNQVNEIMNRYLLIT--TEVERKQ-----LDPPHRRPVQSH 126
DB 221 SKQSIIELEKKIVTATVNNSVLQKQHDLMETVNNLLTWMSTNSAKDPTVAKEDQIS 280
QY 127 GLDCTDIKDTIGSVTKRPSGLYIIHPRESSYFVEVCMQMDYRGGGWTVIQKRIDGIDFQ 186
DB 281 FRDCADYV---QAGFNKSGIYTYINNMPERPKVFCNMVDVNGGWTVIQRHEDGSLDFQ 336
QY 187 RLWCDYLDGFGDLDGEFVLGLKIFIVYNOKNTSFMLYVALESDDTLAVSYDNFMLED 246
DB 337 RGMKEYKMGFGNPSGEYWLGNFIFALTQSR--QYMLRIELMDQGNRAISQYDRFHIGN 394
QY 247 ETRFKMHLGRYSNAGDAFRGLKEDN--ONAMPFSTSDVNDGCRPAC--LVNGOSVK 302
DB 395 EKQYVRLYKLGHTGTAG-----KQSSLIHGADFSYKADNDNCCKCALMLTG----443
QY 303 SCSHLHNKTMWNECGLANLGIHPS---GLLATGIQMGTVTKNNSPYKIKSVSMK 358
DB 444 -----GWFNRCNSANLNGV-YISGPTAKTND 281
QY 359 IR 360
DB 491 IR 492

Search completed: May 22, 2002, 15:07:55
Job time: 167 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:05:13 ; Search time 29.86 Seconds
(Without alignments)
1248.582 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104
Sequence: 1 MMSPSQASLLFLNVCIFICG.....PVKIKSVSMKIRMYNPYRK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	19.7	439	2 I37391	fibrinogen-like pr
2	405.5	19.3	432	2 A27447	cytotoxic T-lympho
3	401.5	19.1	432	2 I56934	fibrinogen-like pr
4	397	18.9	432	2 JN0596	fibrinogen beta ch
5	394.5	18.8	468	1 FGBOB	fibrinogen beta ch
6	375.5	17.8	491	1 FGHUB	fibrinogen beta ch
7	371.5	17.7	437	1 FGHUG	fibrinogen gamma-A
8	371.5	17.7	453	1 FGHUB	fibrinogen gamma-B
9	371.5	17.7	463	2 A38463	fibrinogen beta ch
10	370	17.6	479	2 A25052	fibrinogen beta ch
11	365	17.3	444	2 S05313	fibrinogen gamma-B
12	363	17.3	432	1 FGLMS	fibrinogen gamma-C
13	353	16.8	438	2 A32670	fibrinogen gamma-C
14	350.5	16.7	282	2 A35084	fibrinogen gamma-C
15	348.5	16.6	774	2 A39832	scabrous locus (sc
16	346.5	16.5	328	2 A05299	fibrinogen beta ch
17	337.5	16.0	866	2 D44234	fibrinogen alpha c
18	330	15.7	1356	2 A45445	janusin precursor,
19	329	15.6	334	2 JCS980	fibrinogen alpha c
20	328.5	15.6	641	1 A41932	fibrinogen alpha-I
21	327.5	15.6	1353	1 JH0675	transferrin precurs
22	312	14.8	323	2 A47172	fibrinogen gamma-A
23	311.5	14.8	437	1 FGRGA	fibrinogen gamma-A
24	311.5	14.8	445	1 FGRGB	fibrinogen gamma-B
25	311	14.8	4135	2 T42629	tenascin-X - bovin
26	310.5	14.8	1810	2 A32230	tenascin precursor
27	304.5	14.5	1914	2 T42635	tenascin Y precurs
28	303.5	14.4	326	2 S61517	tenascin-1 precursor
29	302.5	14.4	3566	1 A40701	tenascin-X precurs

30	299	14.2	417	2 S65944	tenascin-X - pig (
31	296	14.1	220	2 S28170	tenascin homolog -
32	295	14.0	326	2 B47172	tenascin-X - mouse
33	286	13.6	860	2 I48839	tenascin-X - pig
34	284.5	13.5	2019	1 J01322	tenascin precursor
35	283.5	13.5	4006	2 T09070	tenascin precursor
36	282.5	13.4	1746	1 S19694	tenascin precursor
37	271	12.9	2201	2 A32160	tenascin-C - human
38	212.5	10.1	463	2 T15876	tenascin-C - human
39	180.5	8.6	915	2 T21773	hypothetical prote
40	180.5	8.6	927	2 T21772	hypothetical prote
41	173	8.2	431	2 T29850	hypothetical prote
42	154.5	7.3	933	2 A31930	cytoactin - chick
43	128.5	6.1	452	2 T26827	hypothetical prote
44	117	5.6	127	2 FC2036	microfibril associ
45	110.5	5.3	4588	2 T28667	dynein beta heavy

ALIGNMENTS

RESULT 1
I37391
fibrinogen-like protein expressed in T lymphocytes (p149) - human
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I37391; S47273
R:Ruegg, C.; Pyleta, R.
Gene 160, 257-262, 1995
A:Title: Sequence of a human transcript expressed in T-lymphocytes and encoding a fib
A:Reference number: I37391; MUID:9536700
A:Accession: I37391
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-439 <RES>
A:Cross-references: EMBL:Z36531; NID:9535184; PIDN:CA85298.1; PID:9535185
A>Note: submitted to the EMBL Data Library, August 1994
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:210-435/Domain: fibrinogen beta/gamma homology <FBG>

Query Match	19.7%	Score 413.5;	DB 2;	Length 439;
Best Local Similarity	30.2%	Pred. No. 8.5e-25;		
Matches 119;	Conservative 61;	Mismatches 147;	Indels 67;	Gaps 15;
QY 34	SSVNVIVEDGSMARDESKNDTVCKEDCE-----ESCQVYKTK 70			
DB 73	SRIVEFEVONLKEIVNSLKKSC-QDCKIQADNDGPRGRLLPSTGAGEVGDNRVR 131			
QY 71	ITREKHFHMCNLDNS---IVSYTRSTKILRMV-----MDEQASLDYLSQVNEIM 120			
DB 132	ELESEVVKLSSELNAKEIVNLHGRLEKLVNMNIENYDVKVNLTFVNSLDGKC 191			
QY 121	NRVLLITTEVFRKQIDFPHRPVOSHGL--DCTDIKDTIGSVTPPGGLVYIHREGSSYP 178			
DB 192	SKC-----PQEOIQSRPVQ-HLIYKDCSDY---AIGKRSSETRYVPDPKNS 237			
QY 179	FEVNCMDYRGGWTVIQRIDGIIIDFQRLMCDYLDGFGDLGFWLGLKRTFYVQNK 238			
DB 238	FEVVCDEMTGSGWTVLQARLDGSTNFTFRWQDYKAGGNLRREFWLGNDKIHLLT--KS 295			
QY 239	TSEFVLVALESEDTLAYASVDNFWLEDETFEFHMLHGRISGANGDAFRGLAKKDONAM 298			
DB 296	KEMILRIDLEDENGEVYALDYDQYVANEFLRYLHVGNNGTGDALR-FNKRYHNHDLK 354			
QY 299	PESTSDVNDGCRACLYNGQSVKSHHKTKGWMFNEGLANLG-IHFFSGKLATG 357			
DB 355	FTTPPKDNDRYPSG-----NCG-LYSSGWMFDACLSANLNGKYYHOKTRYVNG 404			
QY 358	IOWGTW--TKNNSPVKIKSVSMKIRMYNP-YFK 388			
DB 405	IFWGTWPGVSEAHHPGQYKSSFEKAKMMIRPRHK 428			

RESULT 2
A27447
cytotoxic T-lymphocyte-specific protein precursor (clone PT49) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
C:Accession: A27447
R:Koyama, T.; Hall, L.R.; Haser, W.G.; Tonegawa, S.; Salto, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
A:Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
A:Reference number: A27447; MUID:87175527
A:Accession: A27447
A:Molecule type: mRNA
A:Residues: 1-432 <KOT>
A:Cross-references: GB:M16228; NID:g193304; PIDN:AAA37624.1; PID:g387156
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.3%; Score 405.5; DB 2; Length 432;
Best Local Similarity 35.4%; Pred. No. 3.6e-24;
Matches 110; Conservative 43; Mismatches 115; Indels 43; Gaps 13;

QY 98 LNNMDEQA-----SLDLSNQVNELMNRVLLTTEVFRKQD-----PFP 139
DB 137 LNNMDEQA-----SLDLSNQVNELMNRVLLTTEVFRKQD-----PFP 139
QY 140 HRPVSHGL--DCTDIKDTIGSVTPSGLYTHPEGSSYPPEVNCMDYRGGWTVIOK 197
DB 195 SQPVQ-HLIIKNCSD-HYVLG---RRSSGAVRVTPDHRNNSSEYVCDMETGGWTVIOA 249
QY 198 RIDGIIDPQRLMCDYLDGFGDLGFEWGLGKIFYIVNOKNTSPMLYVALESDDTLAYA 257
DB 250 RLDGSTNFTREKMDYKAGFNGLEREFWLGNDIHLTL--KSKEMTLRIDLEDGFGTLTYA 307
QY 258 SYDNFMLEDTEFFFMHIGRGVSGNAGDAFRGLKREDNQNAPEFSDVNDGCRPACLVN 317
DB 308 LYDPFYVANEFLKRYLHIGNYNGTAGDALR-FSRHYNDLRFPTTPDRDNDYPPSG---- 362
QY 318 GQSVKSCSHLNKTKGWMFNECGLANLNG-IHFSCKLATGIGWGTWTKNN--SPVKIKS 374
DB 363 -----NCG-LYSSGQWDFDSCSLANLNGKYYHQKYGKVGNGIFMGTPGINDAOPGGYKS 416
QY 375 VSMKIRRMYNP 385
DB 417 SFQAKMMIRP 427

RESULT 3
156934
fibrinogen-like protein - mouse
C:Species: Mus sp. (mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Dec-1999
C:Accession: I56934
R:Part, R.L.; Fung, L.; Reneker, J.; Myers-Mason, N.; Leibowitz, J.L.; Levy, G.
J. Virol. 69, 5033-5038, 1995
A:Title: Association of mouse fibrinogen-like protein with murine hepatitis virus-induce
A:Reference number: I56934; MUID:95333285
A:Accession: I56934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <RES>
A:Cross-references: GB:S78773; NID:g1042169; PIDN:AAB34823.1; PID:g1042170
C:Genetics:
A:Gene: musfib1p
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.1%; Score 401.5; DB 2; Length 432;
Best Local Similarity 35.0%; Pred. No. 7.3e-24;
Matches 109; Conservative 43; Mismatches 116; Indels 43; Gaps 13;

QY 98 LNNMDEQA-----SLDLSNQVNELMNRVLLTTEVFRKQD-----PFP 139
DB 137 LNNMDEQA-----SLDLSNQVNELMNRVLLTTEVFRKQD-----PFP 139
QY 140 HRPVSHGL--DCTDIKDTIGSVTPSGLYTHPEGSSYPPEVNCMDYRGGWTVIOK 197
DB 195 SQPVQ-HLIIKNCSD-HYVLG---RRSSGAVRVTPDHRNNSSEYVCDMETGGWTVIOA 249
QY 198 RIDGIIDPQRLMCDYLDGFGDLGFEWGLGKIFYIVNOKNTSPMLYVALESDDTLAYA 257
DB 250 RLDGSTNFTREKMDYKAGFNGLEREFWLGNDIHLTL--KSKEMTLRIDLEDGFGTLTYA 307
QY 258 SYDNFMLEDTEFFFMHIGRGVSGNAGDAFRGLKREDNQNAPEFSDVNDGCRPACLVN 317
DB 308 LYDPFYVANEFLKRYLHIGNYNGTAGDALR-FSRHYNDLRFPTTPDRDNDYPPSG---- 362
QY 318 GQSVKSCSHLNKTKGWMFNECGLANLNG-IHFSCKLATGIGWGTWTKNN--SPVKIKS 374
DB 363 -----NCG-LYSSGQWDFDSCSLANLNGKYYHQKYGKVGNGIFMGTPGINDAOPGGYKS 416
QY 375 VSMKIRRMYNP 385
DB 417 SFQAKMMIRP 427

RESULT 4
JN0596
fibrinogen-related protein HFRP-1 precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: JN0596
R:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kitajima, M.; Hirohashi, S.
Biochem. Biophys. Res. Commun. 193, 681-687, 1993
A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related
A:Reference number: JN0596; MUID:93290661
A:Accession: JN0596
A:Molecule type: mRNA
A:Residues: 1-312 <YAM>
A:Cross-references: GB:D14446; NID:g393314; PIDN:BA00336.1; PID:g393315
A:Experimental source: liver
C:Superfamily: fibrinogen beta/gamma homology
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-312/Product: fibrinogen-related protein HFRP-1 #status predicted <MAT>
F:80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.9%; Score 397; DB 2; Length 312;
Best Local Similarity 34.3%; Pred. No. 1.1e-23;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

QY 87 IVSYRSTKRLKLNMMDEQAQSLDLSNQVNELMNRVLLTTEVFRKQ----- 134
DB 4 VSFLLVLTAL--NGREISALEDCADQOMRLRAQVRLLETRVAKQOQVRIKQLOENEV 60
QY 135 --LDPEFHPVQSHG----LDCTDIKDTIGSVTPSGLYTHPEGSSYPPEVNCMDY 187
DB 61 QFLDGDEDTVDLDSKROYADCSSEFNDGYKL----SGFYIKPLQSPAESVYCDMS- 115
QY 188 RCGWTVIOKRIIDGIIDPQRLMCDYLDGFGDL--GEFWGLGKIFYIVNOKNTSPMLY 244
DB 116 DGGWTVIORDSGSENFGRGKQYENGRCNVQKNGEVLGNKMLHLFTQDED--YTLK 173
QY 245 VALESDDTLAYASYDNFMLEDTEFFFMHIGRGVSGNAGDAFRGLKREDNQ-----NMP 299
DB 174 IDLADFEKRSRYAQYKNFEVGDENFELINIGYSGTAGDSLGNFHPHEVQWMAASHQRMK 233
QY 300 FSTSDVNDGCRPACLVNQSVKSCSHLNKTKGWMFNECGLANLNGIHHFSCKLLA---T 356
DB 234 FSTWDRDHNYEGNCAEEDQS-----GWMFNCHSANLNGV-YGSPYTAKTDN 281
QY 357 GIQMGWTVTKNNSPVKIKSVSMKIR 380
DB 282 GLVWYTW--HGMWYSILKSVYMKIR 303

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RESULT 5
FGBOB
fibrinogen beta chain - bovine
N:Contains: fibrinopeptide B
C:Species: Bos primigenius taurus (cattle)
C>Date: 29-Jul-1981 #sequence revision 29-Jul-1981 #text_change 13-Sep-1996
C:Accession: A03122; B03117; B37507; A37513; S02443
R:Blomback, B.; Doolittle, R.F.
Acta Chem. Scand. 17, 1816-1819, 1963
A:Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
A:Reference number: A03122
A:Accession: A03122
A:Molecule type: protein
A:Residues: 1-4 <BLO>
R:Sjogquist, J.; Blomback, B.; Wallen, P.
Ark. Kemi 16, 425-436, 1960
A:Title: Amino acid sequence of bovine fibrinopeptides.
A:Reference number: A03117
A:Accession: B03117
A:Molecule type: protein
A:Residues: 5-21 <SJO>
R:Martinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
Arch. Biochem. Biophys. 192, 27-32, 1979
A:Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
A:Reference number: A37507; M01D:79164394
A:Accession: B37507
A:Molecule type: protein
A:Residues: 22-53 <MAR>
R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
A:Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
A:Reference number: A37513; M01D:81199473
A:Accession: A37513
A:Molecule type: mRNA
A:Residues: 44-468 <CHU>
R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
FEBS Lett. 232, 56-60, 1988
A:Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
A:Reference number: S02443; M01D:88211875
A:Accession: S02443
A:Molecule type: protein
A:Residues: 373-374 <MED>
C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
C:Superfamily: fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
C:Keywords: blood coagulation; glycoprotein; plasma; pyroglyutamic acid; sulfoprotein
F:76-205/Domain: fibrinogen disulfide ring homology <DR>
F:215-464/Domain: fibrinogen beta/gamma homology <FEB>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
F:371/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

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Query Match 18.8%; Score 394.5; DB 1; Length 468;
Best Local Similarity 27.5%; Pred. No. 2,9e-23;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;

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QY 27 CVHSTDSVVNIYEDSNKDESKMDYCKECCSCVYKTKITREKHF--MCNLTQ 84
DB 72 CLHAPDLGLV-----CPTGCKIADPLVROEPIKRSIEDLR 108
QY 85 NSIYSYRSTFK-----LLRNMDQOASLDYLSNOVNELMN----- 121
DB 109 NTYDSVSTSSSTFOYITLKNMKKGRQNOVDENYVNESSLEKHQYIDETVKNNT 168
QY 122 ----RVLLTTEYFRKQDPP-----HRPVSHGLDCTDIKDTGS 159
DB 169 PTKLRVLRSLLENRSKIQKLESDVSTOMEYCRTPCTVTCNIPYVS--GKECEKILRNDE 227

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QY 160 VTKPSGLYIHPESSYPPEVMCDMDYRGSGWTVIQRIKIDGIIIDPQLMCLYDGFGL 219
DB 228 T-----SEMVILOPEDSSKPRVYCDMKTGCGTFTVIONRDDGSLDPFRKMDPYKQGGNI 283
QY 220 L-----GEFWLGKIKFYIVNOKNTSEMLVVALESEDDTLAVSYDNFWLEDE 267
DB 284 ATNAEGKKYCGVEYWLGNDRISQLTNNMGPTK--LLIEMEDMKGDVYALYEGFTVQNE 341
QY 268 TRFFKMLGKRYSGNAGAF-----RGLKKEDN-----QNAPEFSTSDVNDCCPRACLVNGQ 319
DB 342 ANKYQLSVSKYKGTAGALLLEGASQLVGENRMTITNHSNMFSTYDRNDGDKTT-----D 396
QY 320 SVKSCSLHMKGTGWFNEGCLANLNGIHFSGLK-----LATGLOMTWTKNNSPVK 371
DB 397 PKQCSK-EDGGGWYRRCIAANPNNGRYNGAYTWMAGKHGDDGVYWMNW--QGSWYS 453
QY 372 IKSVSMKIRRMYPYF 387
DB 454 MKKSMKIR---PYF 465

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RESULT 6
FGBHB
fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence revision 31-Mar-1993 #text_change 08-Dec-2000
C:Accession: B43568; A90469; B90469; I37389; A94433; A90437; A94309; G54223; A03121;
R:Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A:Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A:Reference number: A43568; M01D:91344740
A:Accession: B43568
A:Molecule type: DNA
A:Residues: 9-191, 'P', 193-491 <CHU>
R:Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A:Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyrib
A:Reference number: A90469; M01D:83283433
A:Accession: A90469
A:Molecule type: DNA
A:Residues: 1-38 <CHU>
A:Accession: B90469
A:Molecule type: mRNA
A:Residues: 9-191, 'A', 193-491 <CH2>
A:Cross-references: GB:J00129; NID:g182429; PIDN:AAA52429.1; PID:g182430
R:Huber, P.; Dalmont, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
Nucleic Acids Res. 15, 1615-1625, 1987
A:Title: Characterization of the 5'-flanking region for the human fibrinogen beta gen
A:Reference number: I37389; M01D:87146483
A:Accession: I37389
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-38 <HUB>
A:Cross-references: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
R:Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
In: Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
A:Reference number: A94433
A:Contents: carbohydrate binding
A:Accession: A94433
A:Molecule type: protein
A:Residues: 31-137, 'OS', 140-144, 'OF', 147-491 <HEN>
R:Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
A:Title: Amino acid sequence of the beta chain of human fibrinogen.
A:Reference number: A90437; M01D:79124640
A:Accession: A90437
A:Molecule type: protein
A:Residues: 31-144, 'OF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
R:Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976

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A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; MUID:76225080
A:Contents: disulfide bonds
A:Accession: A94309
A:Molecule type: protein
A:Residues: 31-112,'E',114-137,'Q',140-144,'Q',147-148 <BLO>
R:Kunitake, S.T.; Carilli, C.T.; Lau, K.; Prother, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipoprotein
A:Reference number: A54223; MUID:941652201
A:Accession: G54223
A:Molecule type: protein
A:Residues: 164-174 <KUN>
A:Note: Identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottepeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; MUID:83254370
A:Contents: annotation; review, disulfide bonds
R:Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
Eur. J. Biochem. 77, 595-610, 1977
A:Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
A:Reference number: A91249; MUID:77245999
A:Contents: annotation; disulfide bonds
R:Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; C
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folth
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Contents: annotation; disulfide bonds
R:Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; MUID:84305751
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Chung, D.W.; Rixon, M.W.; Que, B.G.; Davie, E.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A:Title: Cloning of fibrinogen genes and their cDNA.
A:Reference number: A90038; MUID:83254384
A:Contents: annotation
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH-ter
A:Reference number: A37117; MUID:90337977
A:Contents: annotation; hemetin cleavage site
A:Note: hemetin, a protease from *Haementeria gillmanii*, the giant South American leech,
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Genetics:
A:Gene: GDB:FGH
A:Cross-references: GDB:119130; OMIM:134830
A:Map position: 4q28-4q28
A:Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A:Pathway: blood coagulation
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfid
C:Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic ac
E:1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted <SIG>
E:31-491/Product: fibrinogen beta chain #status experimental <MAT>
E:31-44/Product: fibrinopeptide B #status experimental <APT>
E:45-491/Product: fibrin beta chain #status experimental <FGB>
E:45-47/Region: polymerization site
E:99-228/Domain: fibrinogen beta/gamma homology <PBG>
E:238-487/Domain: fibrinogen disulfide ring homology <RNG>
E:31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
E:44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
E:95/Disulfide bonds: Interchain (to alpha-55) #status experimental

```
F:106/Disulfide bonds: interchain (to alpha-68) #status experimental
F:110/Disulfide bonds: interchain (to gamma-45) #status experimental
F:123/Disulfide bonds: interchain (to alpha-184) #status experimental
F:227/Disulfide bonds: interchain (to gamma-161) #status experimental
F:329-316-241-270,424-437/Disulfide bonds: #status experimental
F:394/Binding site: carbonylate (asn) (covalent) #status experimental
```

Query Match	17.8%	Score 375.5;	DB 1;	Length 491;
Best Local Similarity	26.6%	Pred. No. 9,6e-22;		
Matches 118: Conservative	56;	Mismatches 142;	Indels 127;	Gaps 17;

[illegible]

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RESULT 7
FCRHC
fibrinogen gamma-A chain precursor [validated] - human
N:Alternate names: coagulation factor I
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1994 #sequence_revision 25-Feb-1985 #text_change 08-Dec-2000
C:Accession: A90470; B90494; G94433; B93956; B92448; I37393; A40698; H54223; A03125;
R:Chung, D.W.; Chan, W.Y.; Davie, E.W.
Biochemistry 22, 3250-3256, 1983
A:Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma
A:Reference number: A90470; MUID:83285434
A:Accession: A90470
A:Molecule type: mRNA
A:Residues: 1-437 <CHD>
R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:8525774
A:Accession: B90494
A:Molecule type: DNA
A:Residues: 1113,'T',115-437 <RIX>
A:Cross-references: GB:X02415; GB:M10014; NID:g182438; PIDN:AAB59531.1; PID:g182439
R:Henschel, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
In Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56,
A:Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural
A:Reference number: A94433
A:Accession: C94433
A:Molecule type: protein

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A:Residues: 27-437 <HBN>
R:Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A:Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: ex
A:Reference number: A93956; M0ID:83247396
A:Accession: B93956
A:Molecule type: mRNA
A:Residues: 276-437 <KAN>
R:Porcane, Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; M0ID:85030379
A:Accession: B92448
A:Molecule type: DNA
A:Residues: 286-437 <FOR>
R:Manu, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1993
A:Title: Isolation and characterisation of cDNA clones for the Alpha- and gamma-chains
A:Reference number: 137393; M0ID:84069777
A:Accession: 137393
A:Status: preliminary; translated from GB/EMBL/DBDB
A:Molecule type: mRNA
A:Residues: 209-270 <RES>
A:Cross-references: EMBL:X00086; NID:g31445; PIDN:CAA24944.1; PID:9577055
R:Bernagnoli, M.E.; Beckerle, M.C.
J. Cell Biol. 121, 1329-1342, 1993
A:Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th
A:Reference number: A40698; M0ID:93286185
A:Accession: A40698
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <BER>
A:Experimental source: thrombin-activated platelets
A:Note: sequence extracted from NCBI backbone (NCBI:P.133734)
R:Kuntake, S.T.; Carrilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
A:Title: Identification of proteins associated with apolipoprotein A-I-containing lipop
A:Reference number: A54223; M0ID:94162201
A:Accession: H54223
A:Molecule type: protein
A:Residues: 27-33, 'XX', 36-41 <KUN>
A:Note: Identification of tryptic peptides from high-density lipoproteins
R:Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A:Title: Covalent structure of fibrinogen.
A:Reference number: A90037; M0ID:83254370
A:Accession: A90037
A:Contents: annotation; review, disulfide bonds
R:Doillittle, R.F.; Takagi, T.; Walt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G
in Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
A:Title: The structures of fibrinogen and fibrin.
A:Reference number: A94437
A:Accession: A94437
A:Contents: annotation; disulfide bonds
R:Blomback, B.; Hessel, B.; Hoger, D.
Thromb. Res. 8, 639-658, 1976
A:Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A:Reference number: A94309; M0ID:76225080
A:Accession: A94309
A:Contents: annotation; disulfide bonds
R:Hoepfich, P.D.; Doillittle, R.F.
Biochemistry 22, 2049-2055, 1983
A:Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds
A:Reference number: A90467; M0ID:83231465
A:Accession: A90467
A:Contents: annotation; quaternary structure, disulfide bonds
R:Doillittle, R.F.
Ann. Rev. Biochem. 53, 195-229, 1984
A:Title: Fibrinogen and fibrin.
A:Reference number: A90041; M0ID:84305751
A:Accession: A90041
A:Contents: annotation; review, EM structure, polymerization, ligands
R:Horwitz, B.H.; Varadi, A.; Scheraga, H.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984
A:Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374
A:Reference number: A94006; M0ID:85014892
A:Accession: A94006
A:Contents: annotation; polymerization region
R:Kloczewiak, M.; Timmons, S.; Lukas, T.J.; Hawiger, J.
Biochemistry 23, 1767-1774, 1984

A:Title: Platelet receptor recognition site on human fibrinogen. Synthesis and struct
A:Reference number: A90483; M0ID:84203545
A:Accession: A90483
A:Contents: annotation; platelet aggregation region
R:Plow, E.F.; Stoull, A.H.; Meyer, D.; Marguerite, G.; Ginsberg, M.H.
J. Biol. Chem. 259, 5388-5391, 1984
A:Title: Evidence that three adhesive proteins interact with a common recognition sit
A:Reference number: A92477; M0ID:84185664
A:Accession: A92477
A:Contents: annotation; platelet aggregation region
R:Dang, C.V.; Ebert, R.F.; Bell, M.R.
J. Biol. Chem. 260, 9713-9719, 1985
A:Title: Localization of a fibrinogen calcium binding site between gamma-subunit posi
A:Reference number: A92549; M0ID:85261382
A:Accession: A92549
A:Contents: annotation; calcium binding region
R:Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A:Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH
A:Reference number: A37117; M0ID:90337977
A:Accession: A37117
A:Contents: annotation; hematin cleavage site
A:Note: hementin, a protease from Haemophilia gillanii, the giant South American lee
C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cle
ization sites responsible for the formation of the soft clot.
C:Comment: The soft clot is converted into the hard clot by Factor XIIIa (fibrin-stab
ger) and between alpha chains (weaker) of different monomers.
C:Comment: All fibrinogen chains are synthesized in the liver.
C:Comment: The two forms of gamma chain, A and B (see PIR:FGHGB), arise by alternate
intron, which makes this chain different from the gamma-B chain at positions 434-437
C:Genetics:
A:Gene: GDB:119132; OMIM:134850
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/4; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR
ins are contained in the core. Two three-chain coiled coils emerge from this core and
from the distal domain nodes.
C:Function:
A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-437/Product: fibrinogen gamma-A chain #status experimental <MP>
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>
F:341-355/Domain: calcium binding #status predicted <AB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F:423-437/Region: platelet aggregation #status predicted
F:34/Disulfide bonds: interchain (to gamma-35) #status experimental
F:35/Disulfide bonds: interchain (to gamma-34) #status experimental
F:45/Disulfide bonds: interchain (to beta-110) #status experimental
F:49/Disulfide bonds: interchain (to alpha-64) #status experimental
F:78/Binding site: carbohydrate (asn) (covalent) #status experimental
F:161/Disulfide bonds: interchain (to beta-227) #status experimental
F:165/Disulfide bonds: interchain (to alpha-180) #status experimental
F:179-208, 352-365/Disulfide bonds: #status experimental
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status experimen
F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental

Query Match 17.7%; Score 371.5; DB 1; Length 437;
Best Local Similarity 31.9%; Pred. No. 1.7e-21;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

QY 85 NSIYSYRSTRKLLRNMMDEQ-----QASLDYLSNOVNEIMNRYVLLITTEVFRRKQDPF 138
DB 103 NMIDAATLTKSRKMLEETMKYEASILTHDSSTRYLQELIYNSNNQIKVLEKEV--AQLEAQ 160
QY 139 PHRP-----VQSH---GLDCDIDIKTIGSVTRPGLYIIPEGSSYFEVWCMDYRGCG 191
DB 161 CQEQCKRFPVQIHDTGDCQD---IANKGAKSGILFIRKRNQGFIVYCEIDSGNG 216
QY 192 WTVYQKRIDGIDFQRLWCDYLDGFGDL---LGEFWLGLKRTFYIVNQKTSFMLYVAL 247
DB 217 WTVFQKRIDGSDVPRKKNWIKYEGFGLHSPTGTETFWLGNKIKHLISTQAIPIALRYEL 276

```

Oy 248 ESEDDTLAVASDYNFWLDETFEFKMHGGRYS-GNAGDAFRGLKKED-----NONAM 298
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EDWNRSTADYAMFKRVEPEADKRYLTYAFAGGAGDAFDFGDDPSDKFTSHNGM 336
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 299 PESTSDVDNDGCRPACLVNGOSVSKCSHLHNKTGMWFNECGLANLNGIHFFSGKT----- 353
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 QESTDNDNDKREGCACADQDS-----GWMNKKCHAGHLNGVYGGGTYSKAST 385
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 354 ---LATGIQMGTWTKNNSPVKIKSVSMKI 379
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 386 PNGYDNGIIMATW--KTRWYSMKKTTMKI 412
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
FGHUGB
N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain
C:Species: Homo sapiens (man)
C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text change 08-Dec-2000
C:Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
R:Rixom, M.W.; Chung, D.W.; Davie, E.W.
Biochemistry 24, 2077-2086, 1985
A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
A:Reference number: A90494; MUID:85252774
A:Accession: A90494
A:Molecule type: DNA
A:Residues: 1-113,'T',115-453 <RIX>
A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PIDN:AA5595
R:Formace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
J. Biol. Chem. 259, 12826-12830, 1984
A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
A:Reference number: A92448; MUID:85030379
A:Accession: A92448
A:Molecule type: DNA
A:Residues: 286-453 <FOR>
R:Molienstein-Todel, C.; Moesseson, M.W.
Biochemistry 20, 6146-6149, 1981
A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
A:Reference number: A90453; MUID:82068993
A:Accession: A90453
A:Molecule type: protein
A:Residues: 411-434,'Y',436-440,'Z',442,'Z',444,'B',446-447,'R',449,'ZBB',453 <WOL>
R:Francis, C.W.; Mueller, E.; Henschen, A.; Simpson, P.J.; Marder, V.J.
Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
A:Reference number: A94194; MUID:86217900
A:Accession: A28203
A:Molecule type: protein
A:Residues: 433-449 <FRA>
A:Accession: B28203
A:Molecule type: protein
A:Residues: 453-453 <FR2>
R:Marchetti, L.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
DNA Seq. 1, 419-422, 1991
A:Title: Polymorphism of the human gamma chain fibrinogen gene.
A:Reference number: I37390; MUID:92119334
A:Accession: I37390
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 75-286 <RES>
A:Cross-references: EMBL:X51473; NID:931410; PIDN:CA53837.1; PID:9930064
C:Comment: The two forms of gamma chain, A (see PIR:FGHUG) and B, arise by alternate spli
ntron, which makes this chain different from the gamma-B chain at positions 434-437 and
C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas
C:Genetics:
A:Gene: GDB:FGC
A:Cross-references: GDB:119132; OMIM:134850
A:Map position: 4q28-4q28
A:Introns: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
ins are contained in the core. Two three-chain coiled coils emerge from this core and co
from the distal domain nodes.
C:Function:

```

```

A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized in
A:Pathway: blood coagulation
C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprote
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-453/Product: fibrinogen gamma-B chain #status experimental <MP>
F:176-415/Domain: fibrinogen beta/gamma homology <FBG>
F:341-355/Domain: calcium binding #status predicted <CAB>
F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of
F:34/Disulfide bonds: interchain (to gamma-35) #status predicted
F:35/Disulfide bonds: interchain (to gamma-34) #status predicted
F:45/Disulfide bonds: interchain (to beta-110) #status predicted
F:49/Disulfide bonds: interchain (to alpha-64) #status predicted
F:78/Binding site: carbonyl (asn) (covalent) #status predicted
F:161/Disulfide bonds: interchain (to beta-227) #status predicted
F:165/Disulfide bonds: interchain (to alpha-180) #status predicted
F:179-208,352-365/Disulfide bonds: #status predicted
F:424/Cross-link: isopeptide (Gln) (interchain to Lys-432 N6-amino) #status predicted
F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status predicted

```

```

Query Match 17.7%; Score 371.5; DB 1; Length 453;
Best Local Similarity 31.9%; Pred. No. 1.8e-21;
Matches 105; Conservative 42; Mismatches 129; Indels 53; Gaps 11;

```

```

Oy 85 NSIVSTSTKKLRLNMDEQ-----QASLDYSNQVNLNRYLLTTEVERKQDPF 138
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 NMIDATLTKSRMLEEIMKYEASILTHDSIRYLDEIYSNNQKIVNKEKV--AQLEAQ 160
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 139 PRRP-----VQSH---GLDPTDKDTIGSVTKRPSGLYIIRHPESSYPPEVMDQYRGSG 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 COEPCKDVIYQHIDITGKCDQ----LANKGAQSGILFKPKLAKNOQPLVYEIDSGSNG 216
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 192 WTVIQKRIDGIIIDFORLWCVDYLDGFDL---LGEFWLGLKRTFYIVNOKNTSMILYVAL 247
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 217 WTVPKRLDGSVDPKFKMNIQYKEGFGHLSPGTETFEWLGNEKHILISQSAIPVALRVEL 276
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 248 ESEDDTLAVASDYNFWLDETFEFKMHGGRYS-GNAGDAFRGLKKED-----NONAM 298
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 EDWNRSTADYAMFKRVEPEADKRYLTYAFAGGAGDAFDFGDDPSDKFTSHNGM 336
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 299 PESTSDVDNDGCRPACLVNGOSVSKCSHLHNKTGMWFNECGLANLNGIHFFSGKT----- 353
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 QESTDNDNDKREGCACADQDS-----GWMNKKCHAGHLNGVYGGGTYSKAST 385
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 354 ---LATGIQMGTWTKNNSPVKIKSVSMKI 379
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 386 PNGYDNGIIMATW--KTRWYSMKKTTMKI 412
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 9
A38463
fibrinogen beta chain - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Jul-1991 #sequence revision 31-Jul-1991 #text change 13-Aug-1999
C:Accession: A38463
R:Weissbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
Biochemistry 30, 3290-3294, 1991
A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage
A:Reference number: A38463; MUID:91182745
A:Accession: A38463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-463 <WEI>
A:Cross-references: GB:M58514; NID:9211779; PIDN:AAA48770.1; PID:9211780
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disu
F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

```

```

Query Match 17.7%; Score 371.5; DB 2; Length 463;
Best Local Similarity 27.7%; Pred. No. 1.8e-21;
Matches 112; Conservative 57; Mismatches 136; Indels 99; Gaps 17;

```

```

OY 61 CEESCDVKTKITREEKH--MCENLONISIV--TRSTKLLRNMD-----103
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 80 CPTGCGLOTTLLKQETVAPVLRDLKORVAKESDSTTMQYVAMDNKLVTOKORKDN 139
OY 104 -----EQOASLDYLSNQVNELMNRVLLTTEVERKOLDPEPHRPVOS-----145
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 140 DILSEYNTMEMELHNYIKNDLNDNIPSSLRVLRRAVIDSL-HKIKOLENAIATQTDYCR 198
OY 146 -----HGLDCTDIKDTIGSVTKTPSGLYIIHPEGSSYPREVMCDMDYRGSGWT 193
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 199 SPCVASCNIPVVSGRCEBIYRKGET---SEMYIIQPPFTTPYKRYVCDMEIDNGWMT 254
OY 194 VIQKRDIIGIDFORLWCDVLDGFC-----DLLEGFWLGKIKFIYVNOKNNSFM 242
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 255 LIONRQDGSVNGRANDEYKRGFGNIAKSGKKYCDPGEYIWLGNKISQITIGPTK-- 312
OY 243 LVVALESED--DTLAVASYDNFMLEDETFEFKMLGRYSGNAGDAF---RGLKKEDN- 294
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 313 --VLIMEDMNGDKVS-ALYGGFTIHNEGNKYQLSVSNYGNMGNALMEGASQOLDYGENRT 369
OY 295 ---QNAAPFSTSDVDNDCRPACLVNGQSVKSCSHLHNTGMPNECGLANLNGIHHSFG 351
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 370 MTHNGMYFSTYDRDNDG---WLTTDPKRCQSK-EDGGGMWYNRCHAAPNRGYYWGC 423
OY 352 KL-----LATGIQGTWTKNNSPVKIKSVSMKIRRMVNPYE 387
DB 424 TYSMDAKHGTDDGIYVMMN--KGSWYSMKKMKIK---PYF 461

```

RESULT 10
 A25052
 fibrinogen beta chain - sea lamprey (fragments)
 M/Contains: fibrinopeptide B
 C/Species: Petromyzon marinus (sea lamprey)
 C/Date: 25-Oct-1987 #sequence_revision 19-Feb-1999 #text_change 13-Aug-1999
 C/Accession: A25052; A03124; B03124
 R/Bobonius, V.L.; Doolittle, R.F.; Pontes, M.; Strong, D.D.
 Biochemistry 25, 6512-6516, 1986
 A/Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
 A/Reference number: A25052; MUID:87076582
 A/Accession: A25052

A/Molecule type: mrna
 A/Residues: 39-479 <BOH>
 A/Cross-references: GB:M4773; NID:g213191; PIDN:AAA9261.1; PID:g213192
 R/Cotterell, B.A.; Doolittle, R.F.
 Biochim. Biophys. Acta 453, 426-438, 1976
 A/Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
 A/Reference number: A03120; MUID:77065679
 A/Accession: A03124
 A/Molecule type: protein
 A/Residues: 1-36 <COT1>
 A/Accession: B03124
 A/Molecule type: protein
 A/Residues: 37-42 <COT2>
 C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 C/Keywords: blood coagulation; glycoprotein; sulfoprotein
 F:1-36/Product: fibrinopeptide B #status experimental <FPB>
 F:37-479/Product: fibrin beta chain #status experimental <MAT>
 F:90-219/Domain: fibrinogen disulfide ring homology <FDR>
 F:229-477/Domain: fibrinogen beta/gamma homology <FBG>
 F:13/Binding site: sulfate (Tyr) (covalent) #status experimental
 F:27/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match 17.6%; Score 370; DB 2; Length 479;
 Best Local Similarity 28.9%; Pred. No. 2.5e-21;
 Matches 108; Conservative 63; Mismatches 137; Indels 66; Gaps 17;
 OY 45 NAKDEKSNIDYCKDE-----ESCQVTKITEEKHFKNRNLONSIVSTRS 93
 | :
 DB 130 NSFDRMASDNTLKNQVOTLRRRLNRSSTHVAQKEIENRYEKIR-ISTVAGSLRS 188

```

OY 94 TKLLRNMDQOASLDYLSNQVNELMNRVLLTTEVERKOLDPEPHRPVOSHGLDCTDI 153
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 MKSLVLEHRAKQMEBAIKIQ-KELCSAPCTVACRV-----PVVS-GMRCEDI 235
OY 154 KDTIGSVTKTPPSGLYIIHPEGSSYPFEVMCDMDYRGSGWTVIQKRDIIGIDFORLWCDYL 213
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 236 YRNGGRTSEA---YIOPDLFSEPYKFCFMESHGGSGWTVQNRVDOSSNFARDMNTYK 291
OY 214 DGFDDL-----GEFWLGLKFIYVNOKNNSFMILVALESDDTLAASTDNF 262
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 AEFENIAFGNGKSIQNIPEGEYIIGTITVHQLTKQ-HHQOVLFDMSDMEGSSV-YAOYASF 349
OY 263 WLEDETFEFKMLGRYSGNAGDA-FRGLK--EDNO-----NAMPFSTVDNDCRPAC 314
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 350 RPENEAGYRLWVEDYDGNAGNALLLEGATQLMGDRRTMTINGHOFSTFDNDNWNPF-- 407
OY 315 LVNGQSVKSCSHLHNTGMPNECGLANLNGIHHSFG---KLTA---TGIOGTWTKN 366
| : : : : : : : : : : : : : : : : : : : : : : : :
DB 408 ---GDPTKHCGR-EDAGGMWYNRCHAAPNRGYYWGIYTKEQADYGTDDGVVMMN--K 461
OY 367 NSPVKIKSVSMKIR 380
DB 462 GSWYSMRQAMAKLR 475

```

RESULT 11
 S05313
 fibrinogen gamma-B chain precursor - bovine
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Aug-1999
 C/Accession: S05313
 R/Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.
 Nucleic Acids Res. 17, 6397, 1989
 A/Title: Nucleotide and deduced amino acid sequence of a gamma subunit of bovine fibr
 A/Reference number: S05313; MUID:89366676
 A/Accession: S05313
 A/Molecule type: mrna
 A/Residues: 1-444 <BRQ>
 A/Cross-references: EMBL:X15556; NID:g349; PIDN:CAA33562.1; PID:g350
 A/Note: The authors translated the codon AGT for residue 105 as Ala and ATT for resid
 C/Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-444/Product: fibrinogen gamma-B chain #status predicted <MAT>
 F:114-414/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 17.3%; Score 365; DB 2; Length 444;
 Best Local Similarity 30.2%; Pred. No. 5.6e-21;
 Matches 100; Conservative 51; Mismatches 124; Indels 56; Gaps 12;

OY 85 NSIYSTRSTFKLLRNK-----DEQOASLDYLSNQVNELMNRVLLTTEVERKOLDPE 138
 | :
 DB 101 NNIESATKNSKSMDEIKYETLLSTHSTIRFLQEVYNSNSQKIVNLRDQV--QLEAN 158
 OY 139 PHRPVOS-----HGLDCTDIKDTIGSVTKTPSGLYIIHPEGSSYPFEVMCDMDYRGCG 191
 | :
 DB 159 QCEPCQDTVKNHDTYGRDQD---VANKKAKESGLYTRPL-KAKRPLVCEIDGSSNG 213
 OY 192 WTVIQRIDIGIIDFORLWCDVLDGFGDLL-----GEFWLGLKFIYVNOKNNSFMILYV 245
 | :
 DB 214 WTVFQRKLDGSLDPRKKNWIOYKEGFGHLSPTGNTERMLNENKIHILISTOSSIPYVLRI 273
 OY 246 ALSEEDTLAAASVDNFMLEDETFEFKKNHLGRY-SGNAGDAFRGLAKKD-----NON 296
 | :
 DB 274 QLEDMNGRTSTADYASFVYVTEENDKYRLTYVYFIGDGDADFVDFGDDSSDKFTTSHN 333
 OY 297 AMPFSTVDNDCGRPACLVNGQSVKSCSHLHNTGMPNECGLANLNGIHHSGLLAT 356
 | :
 DB 334 GMQFSTWSDMDKXDGC---AEQV-----GIGMMNKNCHAGHLNGVYUUGGTYSTK 382
 OY 357 -----GIOWGTWTKNNSPVKIKSVSMKI 379
 | :
 DB 383 STPNGYDNGIIMATW--KSRWYSMKKTMTKI 411

Best Local Similarity 36.8%; Pred. No. 4.4e-20;
Matches 92; Conservative 31; Mismatches 96; Indels 31; Gaps 10;

QY 133 KOLDPPHPRVSHGLDCTDIDKDTISVTKTSGLYIIHPGSSYFPEWCDMDYRGCGW 192
DB 58 KRISHSEPP-----RDCYDIIQSC-SGQSPSGQYIIPDGGNL-IKYVCDMETEGGW 110
QY 193 TYIORKRIDIIFORLMCYLDGFGDLGEPWGLKFIPIYVQKMTSEFLYALESEDD 252
DB 111 TYFORRIDGTINFSWSTYOTGFENLNTFELGNDNINHLSQGD--YELRVLNNTLG 168
QY 253 TLAYASYDNFMLEDETRFPMGLGRYSGNAGDAFRLGKKEDNONAMPSTSDVNDGCRP 312
DB 169 NHYAKYNKFRIGDSEFXLLVGAAYSGTAGOSLA-----YHNTMRFSIYDNDND-- 218
QY 313 ACLVNGQSVKSCSH-LHAKTGWMFNDCGLANLNGIHH-FSGKLLATGICWGTWKNNSPV 370
DB 219 -----VYSINCASHSSYGRGAWYKSCLLNLNGQYDYSG---APSIYWSYLPDND-- 268
QY 371 KIKSVSMKIR 380
DB 269 QIPFAEMKLR 278

RESULT 15

A39832
scabrous locus (sca) protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 01-Dec-2000
C:Accession: A39832; S58998
R:Baker, N.E.; Mlodzik, M.; Rubin, G.M.
Science 250, 1370-1377, 1990
A:Title: Spacing differentiation in the developing Drosophila eye: a fibrinogen-related
A:Reference number: A39832; MUID:91075223
A:Accession: A39832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-774 <BAK>
A:Cross-references: GB:M60065; GB:M37703; NID:9158401; PID:9158402
R:Hu, X.; Lee, E.C.; Baker, N.E.
Genetics 141, 607-617, 1995
A:Title: Molecular analysis of scabrous mutant alleles from Drosophila melanogaster indi
A:Reference number: S58998; MUID:96109607
A:Accession: S58998
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-18, 'T', 20-774 <HUX>
C:Genetics:
A:Gene: Flybase:sca
A:Cross-references: Flybase:FBgn0003326
C:Superfamily: fibrinogen beta/gamma homology
F:514-711/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 16.6%; Score 348.5; DB 2; Length 774;
Best Local Similarity 25.1%; Pred. No. 2.3e-19;
Matches 100; Conservative 65; Mismatches 137; Indels 97; Gaps 14;

QY 34 SSVYNIIVEDGSNAKDESKSNDYVCKEDCESDVTKRIT-----REEKHFMCRNLQNSI 87
DB 360 TSMLELELVEVEGIQTMDKSIPELRHEISKLEFANAOITSEQSILIREGTNARSLQAMA 419
QY 88 VSYT-----RSTKLLRNMMDEQASLDYLSQVNEMLNRVL----- 124
DB 420 VSVSYVLOEREGMRKLSAN-VDQLRTNVRLQSLVNDKMKLTHLNKPKRPHQNVQA 478
QY 125 -----LITTEV-----FRKOLDPPHPRVQSHGLDCTDIDKDTIGSVTKT 163
DB 479 QMPQDPSIDSVLAETLVSELENVEYQEAIIINKLRH-----DCSEVH-----TOT 524
QY 164 PSGLYIIHPGSSYFPEWCDMDYRGCGWTVIQRIDGITDFQRLWCXYLDGFGDLGEEF 223
DB 525 -DGLHLIADAGQHRHPLMTGCTAD---GWTTVQRRFDGSADFNRSNADYAQGFAGPGGEF 579

QY 224 WLGIKRIIFYLVNOKNTSFMFLYVALESEDDTLAYASYDNFMLEDETRFPMGLGRYSGNAG 283
DB 580 WIGNEQLHLHT--LDNCSRLQVOMQDIYDNNVWVAEYRFRFYSRADGYRLHIAEYSGNAS 637
QY 284 DAFRLGKKEDNONAMPSTSDVDNDGCRPACLVNGQSVKSCSHLNKTMWFMNCGLANL 343
DB 638 DAL-----NYQSGMPSAIDDDRDIDISQTHCAANYEG-----GWWFSGQHANTL 680
QY 344 NGIHHESGKLLATGICWGTWKNNSPYKIKSVSMKIRRM 382
DB 681 NGRYNTL-----GLTWFDAAARNEM-LAVKSSRLVLRRL 711

Search completed: May 22, 2002, 15:08:30
Job time: 197 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 22, 2002, 15:07:28 ; Search time 49.34 Seconds
(without alignments)
1360.398 Million cell updates/sec

Title: US-09-596-196-4
Perfect score: 2104
Sequence: 1 MMSPQASLLFLNVCIFICG.....PKIKSVSMKIRMYNPK 388

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	427.5	20.3	652	5	Q9NDQ1
2	425	20.2	491	4	Q95841
3	409.5	19.5	357	11	Q9EPT7
4	404.5	19.2	493	11	Q9J03
5	399.5	19.0	489	13	Q90Z18
6	397	18.9	312	4	Q08830
7	397	18.9	312	4	Q96Kw6
8	396.5	18.8	312	4	Q96Kw6
9	390	18.5	498	6	Q9BDY8
10	383.5	18.2	308	5	Q9U8W6
11	382	18.2	495	4	Q9P2Y7
12	380	18.1	346	4	Q43827
13	379.5	18.0	496	11	Q9D2D2
14	378.5	18.0	316	5	Q9U8W7
15	378.5	18.0	407	13	Q9DER1
16	378.5	18.0	488	13	Q91589

17	378.5	18.0	493	13	Q9DER2	Q9DER2 gallus gall
18	376.5	17.9	441	13	Q9DER0	Q9DER0 gallus gall
19	373.5	17.8	496	6	Q9BDY7	Q9BDY7 sus scrofa
20	371.5	17.7	437	4	Q96A14	Q96A14 homo sapien
21	371.5	17.7	453	4	Q96KJ3	Q96KJ3 homo sapien
22	368.5	17.5	407	13	Q9PU54	Q9PU54 gallus gall
23	364.5	17.3	431	6	Q95LU3	Q95LU3 macaca fasc
24	364.5	17.3	513	13	Q90Z19	Q90Z19 brachydanio
25	364	17.3	341	5	Q966W1	Q966W1 halocynthia
26	362.5	17.2	435	13	Q93568	Q93568 gallus gall
27	360	17.1	356	5	Q95P98	Q95P98 halocynthia
28	360	17.1	509	11	Q9WVH6	Q9WVH6 mus musculu
29	359	17.1	244	4	Q9HBP3	Q9HBP3 homo sapien
30	357.5	17.0	932	13	Q57587	Q57587 brachydanio
31	352.5	16.8	592	4	Q95697	Q95697 homo sapien
32	352.5	16.8	1294	4	Q9UOP3	Q9UOP3 homo sapien
33	352	16.7	324	5	Q95PA0	Q95PA0 halocynthia
34	348	16.5	292	5	Q9U8W8	Q9U8W8 tachypneus
35	347	16.5	324	5	Q95P99	Q95P99 halocynthia
36	341	16.2	316	6	Q28529	Q28529 mustela put
37	339	16.1	712	4	Q00531	Q00531 homo sapien
38	339	16.1	1358	4	Q92752	Q92752 homo sapien
39	339	16.1	1358	4	Q15568	Q15568 homo sapien
40	333.5	15.9	372	5	Q18545	Q18545 biophalar
41	333.5	15.9	385	5	Q95UV9	Q95UV9 biophalar
42	332.5	15.7	337	6	Q9HE00	Q9HE00 macaca fasc
43	330	15.7	1356	11	Q05546	Q05546 rattus norv
44	327.5	15.6	235	6	Q28763	Q28763 papio cynoc
45	327.5	15.6	1353	13	Q00546	Q00546 gallus gall

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	652 AA.
Q9NDQ1	Q9NDQ1	Q9NDQ1		
AC	Q9NDQ1	Q9NDQ1		
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	FIBRINOGEN-LIKE PROTEIN.			
GN	CI-FIBRN.			
OS	Ciona intestinalis.			
OC	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Phlebobranchia;			
OC	Cionidae; Ciona.			
OX	NCBI_TaxID=7719;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Hotta K., Takahashi H., Asakura T., Satoh B., Takatori N., Satou Y.,			
RA	Satoh N.;			
RT	"Characterization of Brachyury downstream notochord genes in the Ciona			
RT	intestinalis embryo."			
RL	Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB036849; BAB00626.1; -			
DR	HSSP; P02671; 1E7D.			
DR	InterPro; IPR002181; Fibrinogen_C.			
DR	Pfam; PF00147; Fibrinogen_C; 1.			
DR	SMART; SM00186; FBG; 1.			
DR	PROSITE; PS00514; FIBRIN_AC_C-DOMAIN; 1.			
DR	SEQUENCE 652 AA; 73252 MW; A492BA325162FE00 CRC64;			

Query Match 20.3%; Score 427.5; DB 5; Length 652;

Best Local Similarity 30.7%; Pred. No. 9.1e-28;

Matches 115; Conservative 67; Mismatches 124; Indels 69; Gaps 16;

QY	50	SKSNFTVCK---EDCEESDVKTKTRREKHM-----CRLLQNSIVSYTRS-----	93
DB	233	SENDNDKAEADVTRVETTDRTVGEQVTEDETFSTTSQVTSSTSDVTHENN	352
QY	94	---TKLLRNMMDEQASL-----DYLSSQVNV--ELMNRVLLLTTEVFRRL	135

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Db 353 EAMFTSTYTHAVEYTPKVTISSESGVNIROCVATNETEGIEFTSRILRAT----- 404
QY 136 DPPRHPVOSHGL--DCTDIKDTIGSVYTPPSGLYIIHPEGSSYPPEVWCMDDYRGSGMT 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 NPTPVYDGGTSESLPYDCAELY-----ARGVRSQSGVYDIRP-GTKVMTYVCCDMDTDGGMT 459
QY 194 VIOKRIDGIIDPQRLMCDYLDGFGDLGFEWGLKKIFLY-VNOKRTSMFLYALESEDD 252
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 460 MIOQRIDGIIVNSKGMKSTKNGFDINADHWIGLEKMHHSISNKSRRMELRLINTDWD 519
QY 253 TLAYASYDNFMLEDETRFFKMLGRYSGNADAFRLKKEDNONAMPFSTSDVNDGCRP 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 520 VSHYAVYGVFRIRSECKNQLAKRTGTAGDAL-NYGENYNHHLQPTTFEDRDND----- 574
QY 313 ACLVNGQSVKSCSHLNKTGMFNECCGLANLNGIHHSFG--KLATGIGMTWTK----- 365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 575 -----GYALNGNGRY-RSGWFMNACFANLNG-NYTTGPKGVONGIYWGTYWKLS DST 627
QY 366 NNSPVYKISVSKIR 380
Db 628 SNSRYSFKYDMKVR 642

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RESULT 2

095841 PRELIMINARY: PRT: 491 AA.

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AC 095841:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ANGIOPOETIN Y1 (D0595C2.2) (ANGIOPOETIN-RELATED PROTEIN 1
  PRECURSOR)
GN D0595C2.2 OR ARPL
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RX MEDLINE=99148829; PubMed=10025962;
RA Kim I., Kwak H.J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiotensin family
  protein, angiotensin-3."
RL FEBS Lett. 443:353-356(1999).
RN 12
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
  Yamamoto T., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN 14
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
  Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuno Y.,
  Suda T.;
RT "Molecular cloning and characterization of novel angiotensin-related
  protein (ARPL)."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF107253; AAD19608.1; -
DR EMBL: AL355520; CAC13169.1; -
DR EMBL: AB056476; BAB40691.1; -
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.

```

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KW Signal. 1 23
FT SIGNAL. 24 491
SQ SEQUENCE 491 AA: 56719 MW: 3C4DB8DEFCE7E99 CRC64:

```

Query Match 20.2%; Score 425; DB 4; Length 491;
 Best Local Similarity 26.9%; Pred. No. 1e-27;
 Matches 119; Conservative 64; Mismatches 133; Indels 126; Gaps 14;

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QY 44 SNAKDESKNDYVCCKEDCEECQVKTITRE-EKHRCNCLNLSIYSYRSTKLLRNKM 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 68 TKGQDASTIKDATTMRDLENLADYLSRQKREIDVLDLVVDGONIVNEKLLRKESRNN 127
QY 103 DE-QQASLDYL-----SNQVNELMNRVLLTTE----- 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 128 SRVTQLYQMLNHEIIRKRDNSLELSQENKILNTVTEMLKMATRYELEVKYASLTDLVN 187
QY 130 -----VFRQO---LDP-----PRHPVOSHGL----- 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 NOSVMITLLEEOQLRIFSRQDTHVSPPLVQVYPQHLPSQOYTPGLGNETIORPGYPR 247
QY 149 DCTDIKDTIGSVYTKRP-----SGLYTHNPGSSYPFEV 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 248 DLMRPDPLATSPKSPFKIPRYTFINEGPFKCCQAKKEXGHSVSGITMFKPENSGPMOL 307
QY 182 MCDMDYRGSGWTVIOKRIDGIIDPQRLMCDYLDGFGDLGFEWGLKKIFLYVNOKNTSF 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 308 WCENSIDPQGFWYIOKRTDGSVNFRRMENVKKFGFNIDGEYWLGENIYMLSNQDN--Y 365
QY 242 MLYVALESDDPLAYSYNFMLEDETRFFKMLGRYSGNADAFRLKKEDNONAMPSP 301
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 366 KLTELEWSDKKVYVAEYVSFRLEPSEFYLRLGTYGQGNADSDMMW-----HNGKQFT 419
QY 302 TSDVDNDGCRPACLVNGQSVKSCSHLNKTGMFNECCGLANLNGIHHSFGKLLA--TGI 358
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 TIDRDKD-----MAGNCANRH-KGWMYVNCANSLNGVYRGCHIRSKHQDGI 468
QY 359 QMGVTWKNNSPVKISVSKIR 380
Db 469 FMAEY--RCGSYSLRVQWMIK 488

```

RESULT 3

09EP77 PRELIMINARY: PRT: 357 AA.

```

AC 09EP77:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PROTHROMBINASE FGL2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Rychlik D.F., Chien E., Philippe M.;
RT "FGA2 Expression in the Sprague-Dawley Rat."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF323608; AAG42269.1; -
DR HSSP: P02671; 1FZD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
SQ SEQUENCE 357 AA: 40966 MW: 31183DD9A02EBBA9 CRC64:

```

Query Match 19.5%; Score 409.5; DB 11; Length 357;
 Best Local Similarity 32.0%; Pred. No. 1.4e-26;
 Matches 121; Conservative 50; Mismatches 150; Indels 57; Gaps 15;

```

OY 36 VVNIYEDGSNAKDESKSNDYCKEDCESCDV--KTKITREKHFMCRLNLSIVSYTRS 93
Db 4 VLKEVRLQEAVIDSLKSCQDCKLQADHPDPCNGAFTAD-----NRVOELSESQVNK-57
OY 94 TKKLLRNMDDEQQA-----SL-----DLSNQVNEIMNRYLLTTTEVFR-----132
Db 58 LSSEKNAKKEELQGLQGLLESLQLVNMMNIENYDNKAVANLTSVNSLDSCKFCRQSGEH 117
OY 133 KQLDPEPRPVQSHGLDCTDIKDTIGSYTKTPSGLYIIHPGSSYPEFEVWCDMDYRGSGW 192
Db 118 NQPNVQHLIKY-----DCSDYY-VLG-----KRSSGYRVTPDHRNSSFVYDCDMETTGSGW 169
OY 193 TVICKRIGIIDFQRLMCDYLDGFGDLGFEFMLGLKTFEYVONKNTSFMLVYALESDD 252
Db 170 TVLDARLDGSTNFTRGMDYKAGFENLEREFMLGNCKTHLIT--KSKEMILRLIDLEDPNG 227
OY 253 TLAAVASYDNFWLEDETRFKNHGLRGYSGNADAFRGLKEDNONAMPSTSDVDNDGCRP 312
Db 228 LTLAVAYDQFVAVNEFLKYLRLHGLNYNGTAGDALR-FSRHYNHDLRFFTPDRODRYPS 286
OY 313 ACLVNGOSVKSCHLNKTKGWFNECCGLANLNGIHH--FSGKLIATIGQGTW--TKNN 367
Db 287 G-----NCG-LYSSGWMFACLSANLNGKYNOYRGK--VRNGIFWGTWPGVSOA 334
OY 368 SPVKIKSYMKIRRMYNP 385
Db 335 HPGGYKSFESFKAKKMMIRP 352

RESULT 4
O9J03 PRELIMINARY: PRT: 493 AA.
ID O9J03;
AC O9J03;
DT 01-OCT-2000 (Tremblrel, 15, Created)
DT 01-OCT-2000 (Tremblrel, 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE ANGIORENSIN II TYPE 1A RECEPTOR ASSOCIATED PROTEIN.
OS Rattus norvegicus (Rat). Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSTAR-KYOTO. TISSUE=VASCULAR SMOOTH MUSCLE;
RA Guo D.F., Baranes D., Ono Y., Porter J.P., Abl-Jacode E., Orlov S.N.,
Inagami T.;
RT "ARAP1 is required for recycling and reensensitization of angiotensin II
type 1A receptor."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF159049; AAF80364.1; -.
DR HSSP: P02671; f2FD.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C.1.
DR SMART: SM00186; FBG.1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN.1.
KW Receptor.
SQ
SEQUENCE 493 AA; 57159 MW; 7C37652C472B2341 CRC64;

Query Match 19.2%; Score 404.5; DB 11; Length 493;
Best Local Similarity 27.1%; Pred. No. 5.6e-26;
Matches 108; Conservative 68; Mismatches 118; Indels 105; Gaps 15;

OY 62 EESCDVTKIT-----REEKHFMCRLNLSIVSTRSTKLLRNMDDEQ--A 107
Db 125 KESRMNRSRVQLWQLHETIIRKRDNALESOLEIRILNOTADMLQVSKYKDEHFKQ 184
OY 108 SLDIYSNOVNEIM-----NRVL--LTTTEVFR 132
Db 185 HLDMLAHQSEVIAQLEEHQCRVAPARVPPOPPATPPRVYQPPYINRIINOISTNEIOS 244
OY 133 KO---LDP-FPHRPVQSHGLDCTDIKDTIGSVTKTPSG-----LYII 170

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Db 245 DQNLKVLPSPLTPEPALT-----SLPSSIDKPSGPPRDCLQALEDSHTSSITLV 294
OY 171 HPESSSYPEFEVWCDMDYRGSGWTVIQRKIDIIDFQRLMCDYLDGFGDLGFEFMLGLKTI 230
Db 295 KPEMTNRLMQVWQDQHRHDPGQWTVIQRRLDGSVNEFRMFEYTKQGFNGIDSEYWLGIENI 354
OY 231 FYIYNQKTSFMLVVALESEDDTLAYASYDNFWLEDEFKFKMLHGLRSGNAGDAFRGLK 290
Db 355 YWLTNQN--YKLLVTYMDWSGRVFAFYASFRLPESEYKLRIGRHGAGSFTW-- 410
OY 291 KEDNONAMPSTSDVDNDGCRPACILVNGOSVKSCHLNKTKGWFNECCGLANLNGIHFS 350
Db 411 -----HNGKQFTTLDRDH-----YITG-----NCAH-YQKGGWYVNCASHNLNGVWYRG 455
OY 351 GKLLA---TGQWGTWTKNNSPVKIKSYMKIRRMYNP 386
Db 456 GHYRSRYQDGYVMAEF--RGGSYSILKRYVMIRPNPNF 492

RESULT 5
O90218 PRELIMINARY: PRT: 489 AA.
ID O90218;
AC O90218;
DT 01-DEC-2001 (Tremblrel, 19, Created)
DT 01-DEC-2001 (Tremblrel, 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE ANGIOPOLETIN-2.
GN ANG2.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391693; PubMed=11500985;
RA Pham V.N., Roman B.L., Weinstein B.M.;
RT "Isolation and expression analysis of three zebrafish angiopeletin
genes."
RL Dev. Dyn. 221:470-474 (2001).
DR EMBL: AF379603; AAK83348.1; -.
SQ
SEQUENCE 489 AA; 55785 MW; 3ABAE6278539B33C CRC64;

Query Match 19.0%; Score 399.5; DB 13; Length 489;
Best Local Similarity 28.1%; Pred. No. 1.5e-25;
Matches 114; Conservative 55; Mismatches 131; Indels 105; Gaps 16;

OY 23 VQGNCVHSHSTOSSVYNIYEDGSNAKDESKSNDYCKEDCESCDVKTITREKHFMCRLN 82
Db 107 MERNVIHTQT-----ATMLEIGTNLSQSAEN--TCK-----LTDEYQVLANQTS-----R 150
OY 83 LQNSIVSYSTRSTKLLRNMD-----EQQA 107
Db 151 LEIQLEYSLSSTNRLERQLDQYQVSRNLNKSVMQGRFADMEAKHSRELAQIQEQKQ 210
OY 108 SLDIYSNOVNEIM-----RVLLTTEVFRKQLDPEPR-----RPVQS 145
Db 211 LLELDLRQ-NELVSLLEGEELASSTRNSTLLIQROQASLTDVQQLAMVTHCNDISTPYDK 269
OY 146 HGL--DCTDI-KDTIGSVTKTPSGLYIIHPGSSYPEFEVWCDMDYRGSGWTVIQRKIDG 201
Db 270 EMLKFRDCAELFKSGV-----TENGISILHPNSTQKTKVCDMKTKGGWTVQHRHYD 324
OY 202 IIDFQRLMCDYLDGFGDLGFEFMLGLKTFEYVONKNTSFMLVYALESDDTLAYASYDN 261
Db 325 SVDFNRMDNDYKLGFGDPSGSEHMLGNDVIHLTTTKD--YTLQVHLKDAEESHQVSYQDT 382
OY 262 FWLEDETRFKNHGLRGYSGNAGDAFRGLKEDNONAMPSTSDVDNDGCRPACILVNGOSV 321
Db 383 FYIDEDKRYSLHAKGFSGTAGRT-----SSLTHSGQFSTRKDNDNOC----- 426

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OY 322 KSCSHLHNT-GWMEGCLANLNGIHNF--SGKLATGIOWGTW 363
DB 427 -SCKCAQMATGGMWPEACGSPNLNGIYSGNSNVRKYSIKWY 470

RESULT 6
ID 008830 PRELIMINARY: PRT: 312 AA.
AC 008830:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOPHETICAL 36.4 KDA PROTEIN PRECURSOR.
GN HERP-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93290661; PubMed=8390249;
RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitajima M.,
RA Hirohashi S.;
RT "Molecular cloning and initial characterization of a novel fibrinogen-
related gene, HERP-1."
RL Blochem. Biophys. Res. Commun. 193:681-687(1993).
DR HSBP; P02671; IPI2D.
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; fibrinogen_C_1.
DR SMART: SM00166; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Signal; Hypothetical protein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 312 UNKNOWN PROTEIN.
SQ SEQUENCE 312 AA; 36378 MW; 2330F3D60CDD0BBA8 CRC64;
```

Query Match 18.9%; Score 397; DB 4; Length 312;
Best Local Similarity 34.3%; Pred. No. 1.3e-25;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

```
OY 87 IYSYRSTKLLRNMDQASLDYLSNOVNLNRYLLTTEVRKQ----- 134
DB 4 VESFLVLTALI--MGRISALEDCAOEMRLRAOVRLLETRVXQOQYKIKQLDQENEV 60
OY 135 --LDPEPRHPVQSHG-----LDCTDIKDTIGSVTKPTSGLYIIHPEGSSYPREVMCDMDY 187
DB 61 QFLDKGDEFTVVDLSKROYADCSSEIFNDGYKL-----SGFYKIKPLQSPAEFSYICDMS- 115
OY 188 RGGGWTVIQKRIDGIIDFQRLWCYLDLGRGDL--GEFWLGLKIKFYIVNOKNTSFMLY 244
DB 116 DCGGWTVIQRRSDGSENFNRGKDYENGFGNFVQKHGEVWLGKKNLHFLTQED--YTLK 173
OY 245 VALSEDDTLAASVDNFLEDETRFFKMHILGRYSGNAGDAFRGLKKEDNQ-----NAMP 299
DB 174 IDLADFENKSRAYQKKNFVGDENKFEYELNIGESTAGDSLGNFHPREVQWMAASHQRMK 233
OY 300 FSTSDVNDGCRPACLVNGQSVKCSHLHNKGWMEGCLANLNGIHFGSKLLA---T 356
DB 234 FSTWBRDHNHYGNCNCAEEQS-----GWMFNCRHSANLNGV-YISGPTYAKTDN 281

RESULT 7
ID 096KW6 PRELIMINARY: PRT: 312 AA.
AC 096KW6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
```

```
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HP-041.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=21363035; PubMed=11470158;
RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,
RA Morimoto S., Shiohara K.;
RT "Molecular cloning and functional expression analysis of a cDNA for
RT human heparosucin, a liver-specific protein with hepatocyte mitogenic
RT activity."
RL Blochim. Biophys. Acta 1520:45-53(2001).
DR EMBL: D87342; BAB70690.1; --
SQ SEQUENCE 312 AA; 36407 MW; 0E281F4646FB34CC CRC64;
```

Query Match 18.9%; Score 397; DB 4; Length 312;
Best Local Similarity 34.3%; Pred. No. 1.3e-25;
Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

```
OY 87 IYSYRSTKLLRNMDQASLDYLSNOVNLNRYLLTTEVRKQ----- 134
DB 4 VESFLVLTALI--MGRISALEDCAOEMRLRAOVRLLETRVXQOQYKIKQLDQENEV 60
OY 135 --LDPEPRHPVQSHG-----LDCTDIKDTIGSVTKPTSGLYIIHPEGSSYPREVMCDMDY 187
DB 61 QFLDKGDEFTVVDLSKROYADCSSEIFNDGYKL-----SGFYKIKPLQSPAEFSYICDMS- 115
OY 188 RGGGWTVIQKRIDGIIDFQRLWCYLDLGRGDL--GEFWLGLKIKFYIVNOKNTSFMLY 244
DB 116 DCGGWTVIQRRSDGSENFNRGKDYENGFGNFVQKHGEVWLGKKNLHFLTQED--YTLK 173
OY 245 VALSEDDTLAASVDNFLEDETRFFKMHILGRYSGNAGDAFRGLKKEDNQ-----NAMP 299
DB 174 IDLADFENKSRAYQKKNFVGDENKFEYELNIGESTAGDSLGNFHPREVQWMAASHQRMK 233
OY 300 FSTSDVNDGCRPACLVNGQSVKCSHLHNKGWMEGCLANLNGIHFGSKLLA---T 356
DB 234 FSTWBRDHNHYGNCNCAEEQS-----GWMFNCRHSANLNGV-YISGPTYAKTDN 281

RESULT 8
ID 096OM6 PRELIMINARY: PRT: 312 AA.
AC 096OM6:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:12455).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX Struhsberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC007047; AAH07047.1; --
SQ SEQUENCE 312 AA; 36379 MW; 9297153AEA746C31 CRC64;
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Query Match 18.8%; Score 396.5; DB 4; Length 312;
Best Local Similarity 35.0%; Pred. No. 1.5e-25;

Matches 108; Conservative 41; Mismatches 109; Indels 51; Gaps 11;

QY 102 MDQOASLDYLSNOVNEMLRVLLLTTEVFRKO-----LDPFPHRPVQSHG 147
 Db 16 MGEISIALECCABEQMRRLRQVRLLEFRVQKQVKKIKOLLQENVOFLDGDENTYIDLQ 75
 QY 148 -----LDCTDIDKDTIGSVTPKPSGLYIIHPEGSSYPFEVWCMDMDYRGCGTWTIOKRIDI 202
 Db 76 SKRQVYADCSSTIFNDGKYK-----SGFYKIKRLOSPAESVYCDMS-DGGGTVTYQRRSDGS 130
 QY 203 IDFORLMCDYLDGFGDLL--GEFWLGLKKIFVIYNOKNTSEMLVYALASEDDTLAVASY 259
 Db 131 ENFRNPKMDYENEGFNGFVQKHGEYGLGNKNLHFLTQED--YTLKIDLADFEXKNSRYAOX 188
 QY 260 DNFWMLEDETRFFKMHGGRYSGNAGDAFRGLKKEDN-----NAMPSTSDVNDGCRPAC 314
 Db 189 KNFRVDEKRFYELNIGESYGTAGDSLGNFHPHYQWMAHQRRKSTWDRDHDNEGNC 248
 QY 315 LVNGQSVKSCSHLHNKTMWFNFCGLANLNGIHHSGLLA--TGIONCTWTNKNNSPVK 371
 Db 249 AEDQDS-----GWMFNRCHSANLNGV-YISGPTYAKTDNGIWTW--HGMWYS 294
 QY 372 IKSVSMKIR 380
 Db 295 LKSVVMKIR 303

RESULT 9
 Q9BDY8
 ID Q9BDY8 PRELIMINARY; PRT; 498 AA.
 AC Q9BDY8;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE ANGIOPOETIN 1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NC NCBL_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2153163; PubMed=11230987;
 RA Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
 RT "The angiotensin-II α 2 system in coronary artery endothelium prevents
 RT oxidized low-density lipoprotein-induced apoptosis.";
 RL Cardiovasc. Res. 49:872-881(2001).
 DR EMBL: AF233227; AAK1492.1; -.
 DR HSSP: P02671; 1FZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C-DOMAIN; 1.
 SQ SEQUENCE 498 AA; 57413 MW; A8C1C8EF56061876 CRC64;

Query Match 18.5%; Score 390; DB 6; Length 498;
 Best Local Similarity 26.7%; Pred. No. 9.6e-25;
 Matches 115; Conservative 66; Mismatches 127; Indels 122; Gaps 16;

QY 23 VQGNVHSTDSVYNIIVEDGSNAKDESKSNDYCKEDCEESCDVKTITREKHNFCRN 82
 Db 115 IQQNAVGNHNT-----ATMLELGTSLISQT-----AEQTKRLDVEVQVNLQNSRLQL 163
 QY 83 LQNSIVSY-----TNSTKLLRNMM 102
 Db 164 LENSLSYKLEKOLQOTNELIKIHENKSLLENKILEMEGKHKEELDTLKEEKENLQGLV 223
 QY 103 DEQOASLDYLSNOV-----ELM-----NRVLLTTEVP-----RKOLDPF 138
 Db 224 TRQTYITIOELKOLNRRATTNNSYLOKQOLELMDTGVNLVNLCTKEGYLLKGKKEEVKPF 283
 QY 139 PHRPVQSHGDLCTDIDKDTIGSVTPKPSGLYIIHPEGSSYPFEVWCMDMDYRGCGTWTIOKR 198

Db 284 -----RDCADVY-----QAGFNKSGITYIYINMPEPKVFCNMNDLGGCGWTIOHR 330
 QY 199 IDGILDFQRLMCDYLDGFGDLLGEFWLGLKKIFVIYNOKNTSEMLVYALASEDDTLAVAS 258
 Db 331 EDGSLDFQRCWKKYKKGFEFNPSEYWLGNFIFAITSQR--QYTLRTELMDWEGNRAYSQ 388
 QY 259 YDNFWLEDETRFFKMHGGRYSGNAGDAFRGLKKEDN--QNAFPSTSDVNDGCRPAC-- 314
 Db 389 YDRFHIGNENONRRLYIKAGISGTAG-----KQSLILHGADEFSTADADNDNCMKCAL 441
 QY 315 LVNGQSVKSCSHLHNKTMWFNFCGLANLNGIHHS-----GKLLAGIONCTWTNKNNSPV 370
 Db 442 MLNG-----GWMFDACGPNLNGMFYTAGQNHKL--NLIKWHYF--KGPSY 484
 QY 371 IKSVSMKIR 380
 Db 485 SLRSTYVMIR 494

RESULT 10
 Q908W6
 ID Q908W6 PRELIMINARY; PRT; 308 AA.
 AC Q908W6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE TECHLECTIN-5B ISOFORM.
 OS Tachyplesus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyplesus.
 NC NCBL_Taxid=6853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99398666; PubMed=10468566;
 RA Gokudan S., Muta T., Tsuda R., Koori K., Kawahara T., Seki N.,
 RA Mizuno Y., Mai S.N., Iwanaga S., Kawabata S.;
 RT "Horseshoe crab acetyl group-recognizing lectins involved in innate
 RT immunity are structurally related to fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
 DR EMBL: AB024739; BA084190.1; -.
 DR HSSP: P02671; 1FZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C-DOMAIN; 1.
 SQ SEQUENCE 308 AA; 35156 MW; 36161E65EE77E0BF CRC64;

Query Match 18.2%; Score 383.5; DB 5; Length 308;
 Best Local Similarity 29.5%; Pred. No. 1.8e-24;
 Matches 114; Conservative 45; Mismatches 116; Indels 111; Gaps 15;

QY 9 LFLFVNCIFTCGEVYVGNVYHN-----STDSVYNIIVEDGSNAKDESKSNDYCKEDCEES 64
 Db 8 LSFCLVSLVAVGD-----VHNHAACTVCSLKILDSVSDLPDLAKER----- 50
 QY 65 CDVATKTITREKHNKMCNLDNSIVSTRSTKLLRNMMDEQOASLDYLSNOVNEMLRV 124
 Db 51 -----LATLQNSISCKDAF-----YMETTYNTQNRK-- 77
 QY 125 LLTTEVFRKQLDPRPHRPVQSHG--DCTDIDKDTIGSVTPKPSGLYIIHPEGSSYPFEV 182
 Db 78 -----AEKNGLRPICAA-----TVYQOQGNRTSGIYIMVPLFLNHPISLV 115
 QY 183 CDMYRGCGMTWTIOKRID--GIIDFORLMCDYLDGFGDLLGEFWLGLKKIFVIYNOKNT 239
 Db 116 CDMETAGCGMTVIOQRDFGQPIQNFQWESYXNGFGNLTKEFRLANDIIFVLTNG--D 173
 QY 240 SFMLVYALASEDDTLAVASIDNFWLEDETRFFKMHGGRYSGNAGDAFRGLKKEDNQAMP 299
 Db 174 SVVLRVLDLEDFEGGRYRAEAVERFLVRSIELEYKSFYTYQDADDSI-----SQHNMP 227
 QY 300 FSTSDVNDGCRPACLVNGQSVKSCSHLHNKTMWFNFCGLANLNGI-----IHFSGLL 354

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Db 228 FTTKDRDND-----KKEKNCAEAY-KGGWYNACHSHNLNGMTLRGPHES----- 272
Qy 355 ATGIQMGWTWTKNNSPVKIKSYSMKIR 380
Db 273 AVGVNMYQWRGHNYSLKVS--EMKIR 296

RESULT 11
Q9P2Y7 PRELIMINARY; PRT; 495 AA.
ID Q9P2Y7
AC Q9P2Y7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANGIOPOIETIN-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99126459; PubMed=9927494;
RA Tanaka S., Mori M., Sakamoto Y., Makuuchi M., Sugimachi K.,
RA Wands J.R.;
RT "Biologic significance of angiotensin-2 expression in human
RT hepatocellular carcinoma.";
RL J. Clin. Invest. 103:341-345(1999).
DR EMBL; AB009865; BAA95590.1; -.
DR HSSP; P02671; 1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG-C_DOMAIN; 1.
SQ SEQUENCE 495 AA; 56848 MW; EBFAC35ABF1F08F6 CRC64;

Query Match 18.2%; Score 382; DB 4; Length 495;
Best Local Similarity 26.4%; Pred. No. 4.5e-24;
Matches 110; Conservative 73; Mismatches 138; Indels 96; Gaps 16;

Qy 23 VQGNVHSTSSVYNIYEDGSNAKDESKSNDTVCKEDCESCDVTKIT---TTEE--- 75
Db 112 IQQNAVQNOT---AVMEIGTNLNOT-----AEOTRLTDEAVQVLANOTTLLEQL 160
Qy 76 -KHFRCRN-LQNSIVSYSTRSKL-----LRNMDEQOASL 109
Db 161 LEHSLSTKLEKQILDQTSINKLQDKNSPLEKKVLAEMDKHIIQLQSIKEKQDLQVLY 220
Qy 110 DYLSNQVVELMKNVLLN--TEVERKQ-----LDPPHRYVQSHG 147
Db 221 SKQNSIIELEKKIYATATVNSVLDQKQDHMETVNNLLTWMSTNSKDPYAKKEQISF 280
Qy 148 LDCPTIKDTIGSVTKTPSGVLYIHPEGSSYPREVMCDMDYRGCGMTVYAKRIDIDFOR 207
Db 261 RDCAEVFS-----GHTTGITYLTPNSTEELKATCDMEAGGGWTTIIRRDGQVDFOR 336
Qy 208 LWCDDYLDGFDLLGEFWLGLKFIYVQNKTSFMLVYVALESEDDTLAYASYDNWLEDE 267
Db 337 TWKEKVGFGNSGEYVGNFEVSQLTNOQR--YVLKITHLKMENENAVSLTEHRYLSE 394
Qy 268 TRFFPMHLGRISGNAGDAFRGLKEDNOMAFSTSDVNDGCRPACLVNGQSVKSCSHL 327
Db 395 ELNVRHILHKLGLTAGKI-----SSISOPGNDFTKDGDNKC-----ICKSQM 439
Qy 328 HNKQGMWNEGGLANLNGIH--FSGKLATLGIQMGWTWTKNNSPVKIKSYSMKIR 380
Db 440 LT-GGMWFDACGPNLNGMYTPQRONTNKF--NGIKMYW--KGSYSLKATYTMIR 491

RESULT 12
Q43827 PRELIMINARY; PRT; 346 AA.
ID Q43827
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AC Q43827;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDP6 (ANGIOPOIETIN-LIKE FACTOR) (CDP6 PROTEIN).
GN Df647M16.1 OR CDP6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CORNEA;
RA Peek R., van Gelderen B.E., Bruijnenberg M., Kijlstra A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Baguley C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN, AND MELANOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21318995; PubMed=11426320;
RA Stover C., Endo Y., Takahashi M., Lynch N., Constantinescu C.,
RA Vorup-Jensen T., Thiel S., Friedl H., Hankeln T., Hall R., Gregory S.,
RA Fujita T., Schwaeble W.;
RT "The human gene for mannan-binding lectin-associated serine protease-2
RT (MASP-2), the effector component of the lectin route of complement
RT activation, is part of a tightly linked gene cluster on chromosome
RT 1p36.2-3.";
RL Genes Immun. 2:119-127(2001).
DR EMBL; Y16132; CAAT6078.1; -.
DR EMBL; AL049653; CAB84734.1; -.
DR EMBL; BC001881; AAH01881.1; -.
DR EMBL; AJ300188; CAC1571.1; -.
DR HSSP; P02671; 1F2D.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
SQ SEQUENCE 346 AA; 40018 MW; AEC0A601CC498B43 CRC64;

Query Match 18.1%; Score 380; DB 4; Length 346;
Best Local Similarity 27.9%; Pred. No. 4.2e-24;
Matches 107; Conservative 67; Mismatches 138; Indels 72; Gaps 15;

Qy 14 VCIETGEVQGNVHSTSSVYNIYEDGSNAKDESKSNDTVCKEDCESCDVTKIT- 72
Db 12 LCIFIVAFV-----SHPAWLQKLSKHKTPAQQLKAAN--C---CEEVKEKAVAN 58
Qy 73 -----REKHFMCRNLQNSIVSYSTRSKLRLRMNDEQOASLDYLSNQVVELMNR 122
Db 59 LSSLSELNKKQERDWSVVMQ---VMELESNKRMEERLDAESKYEEMNQIDIMQL 115
Qy 123 VLLTTEVERKQLDPFPRPVQSHGLDCTDIKD--TIGSVTKTPSGVLYIHPEGSSYPF 179
Db 116 AAQVYTQTSADAI-----YDCSSLYQKKRYRISGVYKLRPPDFLGSF-----L 158
Qy 180 EVMCDMDYRGCGWTVIQRIDGIDFORLWCDYLDGFDLLGEFWLGLKFIYVQNKNT 239
Db 159 EYFCDMETSGGGWTTIIRKRSGLVSFYDWMQYKQGFSGINDFWLGNHILHRLSRQPT- 217
Qy 240 SFMLYVALESEDDTLAYASYDNWLEDETRFFKMHILGRISGNAG--DARGLKEDNOMAM 298
Db 218 --RLRVEWEDWEGNLRVAYEYSHFYVGNELNSYRLFGLGYTGVAGDAQLQ-----YHNNT 269
Qy 299 PSTSDVDNDGCRPACLVNGQSVKSCSHLNKQGMWNEGGLANLNGIHFSGR--LLAT 356
Db 270 AFSTKQDNQNC-----LDKCAQL--RKGGYWNCCTDSNLNGVYIRLGEHNKHL 318
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Qy 357 G10GWTMKNKSPVIRKISVSMKIR 380
 Db 319 G1TWYGM--HOSTYSLKRVEMKIR 340

RESULT 13

Q902D2
 ID Q902D2 PRELIMINARY; PRT; 496 AA.
 AC Q902D2
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE 11 DAYS PREGNANT ADULT FEMALE OVARY AND UTERUS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:5031400E18, FULL INSERT SEQUENCE.
 GN AGPT2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=OVARY, AND UTERUS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Boffelli D., Bolunga N., Carlini P., de Bonaldo M.F., Blake J., Boffelli D., Bolunga N., Carlini P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontsuki S., Hayaishizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK019860; BAB31887.1;
 DR HSSP: P02671.1FZD.
 DR MGD: MGI:1202890; Agpt2.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FBG.1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN.1.
 SQ SEQUENCE 496 AA; 56575 MW; E7563B498A0EF331 CRC64;

Query Match 18.0%; Score 379.5; DB 11; Length 496;
 Best Local Similarity 25.7%; Pred. No. 7.4e-24;
 Matches 111; Conservative 71; Mismatches 125; Indels 125; Gaps 16;

Qy 23 VQGCYVHSDSSVNVIVEGSSNAKDESKSNDTYCKEDCESCYVKRTITREKHNFCRN 82
 Db 112 IQQWVYQNT---AVVIEGTSLNQTAA-----QTRLTVEVAQVNLQTRRLLEQL 160
 Qy 83 LQNSIVYSTRKTLKLNMMDEQASLDYLSNOVNLNRYLLTTEVF----- 131
 Db 161 LQHSI-----STNKLKQIIDD-----TSEINKLNKKSFLQKVLMEGRHSQDL 207
 Qy 132 -----RKQ---LDPPHRYV-----OSHGIDCTDIKDTIGSVTK-- 162
 Db 208 SMKEQKDELQVLVSGSSVIDELKRLVTAFTVNSLSLQKQOH-----DIWETVNSLLTMM 262
 Qy 163 -----TPSGLYIIHPGSSYPPEVCKMDIRYGGGW 192
 Db 263 SSPNSKSSVAIRKEEQTTFRDCAIEFKSLTTSGLTSTYTLTPNPSTEELKAYCDMDVGGGW 322

Qy 193 TVIQKRIDGIIDPQRLMCDYLDGFGDILGEFNLGKIKFYIVNQKNISFNLVLESDD 252
 Db 323 TVIQREDGSDVDFQRTWKEVKEGFSPLGEYWLGNFVSQLTGHR--YVTKIQKDMEG 380
 Qy 253 TLVAYASVDNFWLEDETRFKKHLGRYSGNAGDAEFGKLEKEDNONAMPSTSDVNDGCRP 312
 Db 381 NEAHSIVDHFELAGEESNYRIHLTGILGTACKI-----SSISQPGSDSTSDSDNDC-- 433
 Qy 313 ACLVNGOSVSKCSHLINKTGMWFMNCGLANLNGHH-----FSGKLATG10GWTMKNNS 368
 Db 434 -----ICKSQMSL--GWMFPDAGCPNSLNGCYPPQKQNTNKF--NGIKWYV--KGS 480
 Qy 369 PVKIKSVSMKIR 380
 Db 481 GYSLKATTMTR 492

RESULT 14

Q908W7
 ID Q908W7 PRELIMINARY; PRT; 316 AA.
 AC Q908W7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE TECHYLECTIN-5B
 OS Tachyleus tridentatus (Japanese horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Tachyplesus.
 OX NCBI_Taxid=6853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9398666; PubMed=10468566;
 RA Gokunoe Y., Muta T., Tsuda R., Koori K., Kawahara T., Seki N., Mizunoe Y., Wai S.N., Iwanaga S., Kawabata S.
 RT "Horseshoe crab acetyl group-recognizing lectins involved in innate immunity are structurally related to fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10086-10091(1999).
 DR EMBL: AB024738; BAB48189.1;
 DR HSSP: P02671.1FZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C.1.
 DR SMART: SM00186; FBG.1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN.1.
 SQ SEQUENCE 316 AA; 36112 MW; 6FEBFED4159EDF1D CRC64;

Query Match 18.0%; Score 378.5; DB 5; Length 316;
 Best Local Similarity 29.3%; Pred. No. 5e-24;
 Matches 113; Conservative 45; Mismatches 117; Indels 111; Gaps 15;

Qy 9 LFLNVCFTIGEVQNCVHH---STDSSVNVIVEGSSNAKDESKSNDTYCKEDCES 64
 Db 16 LFLNVCFTIGEVQNCVHH---STDSSVNVIVEGSSNAKDESKSNDTYCKEDCES 58
 Qy 65 CDVATKITREKHNFCRNLSIVSTRSTKLLRNMMDEQASLDYLSNOVNLNRYLL 124
 Db 59 -----LATLQNPICSKDAF-----YMETYNTYONK-- 85
 Qy 125 LITTEVERKQLDPPRHRYQSHGL--DCTDIKDTIGSVTKTPSGLYIHPGSSYPPEV 182
 Db 86 -----AEKNGLPINCA-----IVYQCGNNTSGIYMWPLFLNHPISVF 123
 Qy 183 CDMDYRGGMVYQKRID---GIIDPQRLMCDYLDGFGDILGEFNLGKIKFYIVYVNO 239
 Db 124 CDMDYRGGMVYQKRID---GIIDPQRLMCDYLDGFGDILGEFNLGKIKFYIVYVNO 239
 Qy 240 SFMLVVALESDDTLAAASYNFMWLEDETRFKKHLGRYSGNAGDAEFGKLEKEDNONAMP 299
 Db 182 SVTLRVLDLEDFEGGRRAEAVEFLVRSIELYKKSFTYKKDAGDSL-----SOHNMP 235
 Qy 300 FSTSDVDNDGCRPACLVNGOSVSKCSHLINKTGMWFMNCGLANLNGI-----HHFSGKL 354

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 22, 2002, 15:07:58 ; Search time 17.4 Seconds

(without alignments)
863.401 Million cell updates/sec

Title: US-09-596-196-4

Perfect score: 2104

Sequence: 1 MMSPSQASLFLANVCIFTCG.....PVKIKSVSMKIRMYNPFYK 388

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	413.5	19.7	439	1 FGL2_HUMAN	Q14314 homo sapien
2	405.5	19.3	432	1 FGL2_MOUSE	P12804 mus musculu
3	400.5	19.0	481	1 AGR1_BOVIN	018920 bos taurus
4	400.5	19.0	493	1 ANL2_MOUSE	09r045 mus musculu
5	400	19.0	493	1 ANL2_MOUSE	09r045 mus musculu
6	398	18.9	312	1 FGL1_HUMAN	Q08630 homo sapien
7	395.5	18.8	468	1 FIBB_BOVIN	P02676 bos taurus
8	395	18.8	498	1 AGR1_HUMAN	Q15389 homo sapien
9	391	18.6	498	1 AGR1_MOUSE	008538 mus musculu
10	381.5	18.1	496	1 AGR2_HUMAN	015123 homo sapien
11	375.5	17.8	491	1 FIBB_HUMAN	P02675 homo sapien
12	375	17.8	375	1 AGR2_BOVIN	077802 bos taurus
13	374.5	17.8	496	1 AGR2_MOUSE	035608 mus musculu
14	373.5	17.8	479	1 FIBB_RAT	P14480 rattus norv
15	371.5	17.7	463	1 FIBB_CHICK	002020 gallus gall
16	370	17.6	477	1 FIBB_PETMA	P02678 petromyzon
17	367.5	17.5	453	1 FIBG_HUMAN	P12799 bos sapien
18	365	17.3	444	1 FIBG_BOVIN	P02679 bos taurus
19	363	17.3	432	1 FIBG_PETMA	P04115 petromyzon
20	360	17.1	509	1 AGR4_MOUSE	Q9wv46 mus musculu
21	358	17.0	503	1 AGR4_HUMAN	Q9y674 homo sapien
22	353	16.8	438	1 FIBG_XENLA	P17634 xenopus lae
23	351	16.7	319	1 FCN2_RAT	P57756 rattus norv
24	350.5	16.7	282	1 FIBB_PARPA	P19477 parastichop
25	348.5	16.6	774	1 SCA_DROME	P21620 drosophila
26	337.5	16.0	866	1 FIBB_HUMAN	P02671 homo sapien
27	335.5	15.9	741	1 FIBB_CHICK	P14448 gallus gall
28	332	15.8	306	1 FCN2_MOUSE	070497 mus musculu
29	329.5	15.7	641	1 FIB2_PETMA	P33573 petromyzon
30	329	15.6	334	1 FCN1_MOUSE	070165 mus musculu
31	327.5	15.6	445	1 FIBG_RAT	P02880 rattus norv
32	321.5	15.3	313	1 FCN2_HUMAN	Q15485 homo sapien
33	321	15.3	255	1 MFA4_HUMAN	P55083 homo sapien

34	313.5	14.9	782	1 FIBB_RAT	P06399 rattus norv
35	310.5	14.8	1808	1 FCN1_CHICK	P10039 gallus gall
36	305.5	14.5	335	1 FCN1_RAT	09wv58 rattus norv
37	303.5	14.4	326	1 FCN1_HUMAN	000602 homo sapien
38	302.5	14.4	4289	1 FCN3_HUMAN	P22105 homo sapien
39	291	13.8	299	1 FCN3_HUMAN	075636 homo sapien
40	282.5	13.4	1746	1 TENA_PIG	029116 sus scrofa
41	271	12.9	2201	1 TENA_HUMAN	P24821 homo sapien
42	197	9.4	137	1 AGR2_RAT	Q35462 rattus norv
43	109	5.2	129	1 MFA4_BOVIN	P55918 bos taurus
44	99.5	4.7	586	1 PMEL_ARATH	Q43867 arabidopsis
45	99	4.7	599	1 YAOB_SCHPO	Q10110 schizosacch

ALIGNMENTS

```

RESULT 1
FGL2_HUMAN          STANDARD:      PRT:   439 AA.
ID      FGL2_HUMAN
AC      Q14314;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Fibrinogen precursor (Fibrinogen-like protein 2) (PT49).
GN      FGL2
OS      Homo sapiens (human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Small intestine;
RX      MEDLINE=95369700; PubMed=7642106;
RA      Ruegg C., Pytela R.;
RT      "Sequence of a human transcript expressed in T-lymphocytes and
RT      encoding a fibrinogen-like protein.";
RL      Gene 160:257-262(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Ywaraaj S., Liu M., Marsden P., Levy G.;
RT      "Cloning and characterization of Hfg12: the human counterpart to the
RT      mouse gene Fgl2.";
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN      [3]
RP      CHARACTERIZATION.
RX      MEDLINE=98309432; PubMed=9647217;
RA      Marazzi S., Blum S., Hartmann R., Gundersen D., Schreyer M.,
RA      Argreaves S., von Fliedner V., Pytela R., Ruegg C.;
RT      "Characterization of human fibrinogen, a fibrinogen-like protein
RT      secreted by T lymphocytes.";
RL      J. Immunol. 161:136-147(1998).
CC      - FUNCTION: MAY PLAY A ROLE IN PHYSIOLOGIC LYMPHOCYTE FUNCTIONS AT
CC      MUCOSAL SITES.
CC      - SUBUNIT: HOMOTETRAMER, DISULFIDE-LINKED.
CC      - SUBCELLULAR LOCATION: Secreted.
CC      - TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN CYTOTOXIC
CC      T-CELLS.
CC      - SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      EMBL: Z36531; CAA85298.1; -
CC      EMBL: AF104015; AAD10825.1; -
CC      EMBL: AF104014; AAD10825.1; JOINED.
CC      HSSP: P02671; LFZD.
CC      MIM: 605351; -

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FT CARBOHYD 294      294          N-LINKED (GLCNAC... ) (POTENTIAL).
FF NON_TER   481     481
SQ SEQUENCE    481 AA; 53556 MW; 8BEC9ED84FC2BB50 CRC64;

Query Match              19.0%; Score 400.5; DB 1; Length 481;
Best Local Similarity 27.9%; Pred.No.1.8e-24;
Matches 114; Conservative 60; Mismatches 116; Indels 119; Gaps 15;

OY 23 VQGNVCNHSSTDSVVAIVIEDGSSNADESKSNDTWCKEDECSCDVKTATTEEKHFMCRN 82
DB :| | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB IIGNNVNQHNT-----ATMLEIGTSLSLQT-----AEQTRKLTIDETGYLVNOTSLRELQL 163

OY 83 LONISLY-----TRSTKLRLRMM 102
DB :| ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB LENSTSYFKLEKKLLQQTNELIKHEKNLSLEHKIFEMEGRHKEEIDLTKEEKENLOGLY 223

OY 103 DEQAQSLDIYSKVQN-----ELM-----NVLLTLTYDF-----RKOLDPEF 139
DB 224 TRQYTIIQELESQRILRRATTNSVLQKOOLEMDVIYNHLVINLCETEVELLKGGKRVEEPF-- 282

OY 140 HRPVSQHGDLCDTDKITDTGSVTYKPFGSGYLIIHPGSSYPFEVMCMDDRGGWITYOKRI 199
DB 283 -----RDCAADV-----QAGFNKSIGITTIYINMPERPKAYPCDMDLNGGMWYIQHRE 330

OY 200 DGIIDFORLMICYDLDFGDLLGEFWLGAKIFYIVNQRTSFMLYVALESDPTLAASY 259
DB |||||::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||}
DB 331 DGSLDPQGOMKEYKGKGFNPSEGYWLGNDEFIALTSQR--QYTLIRIELDWEGNRAYSQY 388

OY 260 DNFMLEDERTFRFKMKLGRXSNAGNAGAFLGKKEDN--ONAPFSFDVDNDGCPRAC--L 315
DB 389 DFHTGHNEKONYTRLVKCHTGTFAG-----KQSSLIHGAADFSTKDINDCNCCKCALM 441

OY 316 VWGQGVKSCSHLNKTMWMNFCECLANINGTHPS----GKLALGIOW 360
DB 442 LTG-----GWWFDCGPSNLNMGMTTAGQNHGKL--NGIKRW 475

RESULT         4
ANL2_MOUSE ANL2_MOUSE STANDARD: PRT; 493 AA.
AC O9R045;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Angiotensin-related protein 2 precursor (Angiotensin-Ilike 2).
GN ANGPT2 OR ARP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NM_1_Taxid=10090; [1]
RN RP SEQUENCE FROM N.A..
RC TISSUE=Heart;
RA MEDLINE=99403103; PubMed=10473614;
RX Kim J., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiotensin-
RT related protein. angiotensin-related protein induces endothelial cell
RT sprouting." ;
RL J. Biol. Chem. 274:26523-26528(1999).
CC -! FUNCTION: INDUCES SPROUTING IN ENDOTHELIAL CELLS THROUGH AN
CC AUTOCRINE AND PARACRINE ACTION (BY SIMILARITY).
CC -! SUBCELLULAR LOCATION: Secreted (By similarity).
CC -! TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND
CC SKLETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS
CC AND TESTIS.
CC -! SIMILARITY: CONTAINS 1 FIRINOGEN C-TERMINAL DOMAIN.
CC -----
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DE related protein 1) (HFEPP-1) (Hepassocin) (HP-041).

GN FGL OR HFEPP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=93290661; PubMed=8390249;

RA Yamamoto T., Gotoh M., Sasaki H., Terada M., Kitaajima M.,

RA Hirohashi S.;

RT "Molecular cloning and initial characterization of a novel

RT fibrogen-related gene, HFEPP-1.";

RL Biochem. Biophys. Res. Commun. 193:681-687(1993).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=21363035; PubMed=11470158;

RA Hara H., Yoshimura H., Uchida S., Toyoda Y., Aoki M., Sakai Y.,

RA Morimoto S., Shikawa K.;

RT "Molecular cloning and functional expression analysis of a cDNA for

RT human hepascocin, a liver-specific protein with hepatocyte mitogenic

RT activity.";

RL Biochim. Biophys. Acta 1520:45-53(2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Has hepatocyte mitogenic activity.

CC -1- SUBUNIT: Homodimer (probable).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Liver-specific.

CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.

CC -----

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CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL: D14446; BAA03336.1; -

DR EMBL: D87342; BAB70690.1; -

DR EMBL: BC007047; AA07047.1; -

DR MIM: 605776; -

DR HSSP: P02671; 1F2D.

DR InterPro: IPR002181; Fibrinogen_C.

DR Pfam: PF00147; fibrinogen_C.1.

DR SMART: SM00186; FBG.1.

DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.

KW Signal.

FT SIGNAL. 1 22

FT CHAIN. 23 312 FIBRINOGEN-LIKE PROTEIN 1.

FT DOMAIN. 78 305 FIBRINOGEN C-TERMINAL.

FT DISULFID. 26 26 INTERCHAIN (POTENTIAL).

FT DISULFID. 83 112 BY SIMILARITY.

FT DISULFID. 248 261 BY SIMILARITY.

FT CONFLICT. 15 15 I -> T (IN REF. 3).

FT CONFLICT. 69 69 N -> D (IN REF. 1).

FT CONFLICT. 72 72 I -> V (IN REF. 1).

FT CONFLICT. 105 105 P -> L (IN REF. 2).

FT CONFLICT. 312 AA; 36391 MW; 26BC82124E660C2 CRC64;

SQ SEQUENCE

Query Match 18.9%; Score 398; DB 1; Length 312;

Best Local Similarity 34.3%; Pred No. 1.6e-24;

Matches 111; Conservative 44; Mismatches 115; Indels 54; Gaps 12;

OY 87 IVSYRSTRKLLRNMMDEQASIDYLSNOVLEMLNVLTLTTEVFRKQ----- 134

: | : | : : : : : | | | | |

Db 4 VFSFILVLTAL---MGRISALEDCAQEQMRLRAQVRLLETRVKKQOVKIKOLQENEV 60

OY 135 --LDPPFHRVYOSH-----LDCTDKDTIGSYTKPISGLYIIHPBGSSIPFEYCMCMDY 187

Db 61 QFIDKRGDENIVIDIGSKROYADCSSEIFNDYKLT---SGFYKIKPLOSFAFSSYCCMS- 115

OY 188 RGGGWTVIORKRIDIGIDFOLMCDYLDGFGDL---GEFMYGLKKIPIYINOKTSMPLY 244

Db 116 DGGGWTVIQRSDGSENFNGMKDYENGFGFVQKCEYWLGNKLNFLTTOED--YTLK 173

OY 245 VALESEDDTLAYASYDNFWEDETRFEKMLHGRYSNAGDAFRGLKEDNQ-----NAMP 299

Db 174 IDLADFENKSRAYQYKFKVGDENKFEYELNIGESYGTAGSLAGNPFPEVQWNASHQRMK 233

OY 300 FSTSDVNDCCRPACLYNGQSVKCSHLAKTKGWMECEGLANINGHHFSKLLA---T 356

Db 234 FSTWDRHDHVEEGNCAEDDS-----GWFNFRCHSANLNGV--YSGPYTAKTDN 281

OY 357 GIOWGTWTKNNSPVKIKSVSMKIR 380

Db 282 GIWVYTW--HGMYSLKSVYMKIR 303

RESULT 7

FIBR_BOVIN STANDARD; PRT; 468 AA.

ID P02676;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Fibrinogen beta chain precursor [contains: Fibrinopeptide B].

GN FGB.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OX Bovidae; Bovinae; Bos.

NCBI_TaxId=9913;

RN [1]

RP SEQUENCE OF 1-4.

RA Blomback B., Doilittle R.F.;

RT "The sequence of amino acids at the N-terminal end of bovine

RT fibrinopeptide B.";

RL Acta Chem. Scand. 17:1816-1819(1963).

RN [2]

RP SEQUENCE OF 5-21.

RA Stojquist J., Blomback B., Wallen P.;

RT "Amino acid sequence of bovine fibrinopeptides.";

RL Ark. Kemi 16:425-436(1960).

RN [3]

RP SEQUENCE OF 22-53.

RX MEDLINE=79164394; PubMed=434821.

RA Martinielli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,

RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;

RT "Amino acid sequences of portions of the alpha and beta chains of

RT bovine fibrinogen.";

RL Arch. Biochem. Biophys. 192:27-32(1979).

RN [4]

RP SEQUENCE OF 44-468 FROM N.A.

RX MEDLINE=81199473; PubMed=6262803;

RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;

RT "Characterization of a cDNA clone coding for the beta chain of bovine

RT fibrinogen.";

RL Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).

CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPOLYMER IN PLATELET

CC AGGREGATION.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

CC THROMBIN, WHICH CLEAVES FIBRINOGEN PEPTIDES A AND B FROM ALPHA & BETA

CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS

CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE

CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: V00110; CAA23444.1; .
CC PIR: A03122; FGBOB.
CC HSSP: P02675; 1FZA.
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C. 1.
CC SMART: SM00186; FBG: 1
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN: 1.
CC Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
CC PEPTIDE 1 21
CC CHAIN 22 468
CC MOD.RES 1 1
CC MOD.RES 6 6
CC SITE 21 22
CC CLEAVAGE (BY THROMBIN; RELEASE
CC FIBRINOPEPTIDE B).
CC FT DISULFID 72 72
CC INTERCHAIN (WITH ALPHA).
CC FT DISULFID 83 83
CC INTERCHAIN (WITH ALPHA).
CC FT DISULFID 87 87
CC INTERCHAIN (WITH GAMMA).
CC FT DISULFID 200 200
CC INTERCHAIN (WITH ALPHA).
CC FT DISULFID 204 204
CC INTERCHAIN (WITH GAMMA).
CC FT DISULFID 208 293
CC BY SIMILARITY.
CC FT DISULFID 218 247
CC BY SIMILARITY.
CC FT DISULFID 401 414
CC BY SIMILARITY.
CC FT CARBOHYD 371 371
CC N-LINKED (GLCNAC. . .) (PROBABLE).
CC SEQUENCE 468 AA; 53340 MW; 2DED42F443AA4B37 CRC64;

Query Match 18.8%; Score 395.5; DB 1; Length 468;
Best Local Similarity 27.5%; Pred. No. 4.3e-24;
Matches 120; Conservative 54; Mismatches 145; Indels 117; Gaps 16;

QY 27 CVHSHDSSVNVIVEDSNKDESKNDYCKEDCESDVCKITREKHF--MCRNLO 84
DB 72 CLHADPLDGLV-----CPTGCKLDPTLVQERPIRKSIEDLR 108
QY 85 NSIYSYSTRSK-----LNRNMDEQOASLDYLSNOVNELMN----- 121
DB 109 NTYDSVSRSSSTFOYTTLLKNNMKGRNOVODNENYVNSSHLEKHQLYIDETVKNKI 168
QY 122 ----RVLLTTEVERKQLDPP-----HRVQSHGLDCTDIKDTIGS 159
DB 169 PTKRLVRLSILENRSKIOLKLESVDSTQMEYCRPTCTVTCNIPYVS--GKECEKIIIRNCE 227
QY 160 VTKPSPGLIIHPESSSYPEVMDMDYRGSGVTVIQKRIDGIIIDFORMCDYDGRDL 219
DB 228 T-----SEMYLLQRPDSSKPYRVYCDMKTERTGKGVVIONROGGSVDFGKWPYQGFRTI 283
QY 220 L-----GEFMGLAKTIPIYIVNOKNTSFMLYVALESEDDTLAAYSDNFWLEDE 267
DB 284 ATNAEGKKYCGVPEYVGLNDRIISQLTNMGPTK--LLIEMDMKGDVYTALEYGFYQNE 341
QY 268 TRFFKMLHGRYSNAGAF-----RGLKEDN-----QNAPESTSDVDNDCRPACLVNGQ 319
DB 342 ANKYQLSVSKYKGTAGNALLEGASQLVGENRTMTIHNSMFSTYDRDNDGKKT-----D 396
QY 320 SVKSCSHLHKTKGMWMECCGANLNGIHHSGL-----LATGLOMGVTWTKNSPYK 371
DB 397 PRKQCSK-EDGGGMMYRCHAANPNGRYVWCGAYTWMADKHTDGDGVVMMW--QGSWYS 453
QY 372 IKYSMKIRRMYNPYF 387
DB 372 IKYSMKIRRMYNPYF 387

DB 454 MKKSMKIR----PYF 465

RESULT 8
ACPL HUMAN
ID ACPL HUMAN STANDARD; PRT; 498 AA.
AC 015389;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Angiotensin-1 precursor (ANG-1).
GN ANGP1 OR KIAA0003.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A. AND VARIANT GLY-269 DEL.
RC TISSUE=Fetal Lung;
RX MEDLINE=97134663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Maisonspierre P.C.,
RA Yancopoulos G.D.;
RT "Isolation of angiotensin-1, a ligand for the TIE2 receptor, by
RT secretion-trap expression cloning.";
RL Cell 87:1161-1169(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Ohara O., Nagase T., Kikuno R., Nomura N.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 307-498 FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. I.
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT analysis of randomly sampled cDNA clones from human immature myeloid
RT cell line KG-1.";
RL DNA Res. 1:27-35(1994).
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PPM: GLYCOSYLATED.
CC -1- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
CC IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
CC PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
CC ISCHEMIC HEART.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL: U83508; AAB50557.1; .
CC EMBL: D13628; BAA02793.2; ALT_INIT.
CC HSSP: P02671; 1FZD.
CC MIM: 601667; .
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C. 1.
CC SMART: SM00186; FBG: 1.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN: 1.
CC Glycoprotein; Coiled coil; Signal; Polymorphism.


```

RT secretion-trap expression cloning."
RL Cell 87:1161-1169(1996).
CC -i- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIAL AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT. AT E9 TO E11, IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -i- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL; U83509; AAB50558.1; -.
CC DR HSSP; P02671; IPZD.
CC DR MGD; MG1:108448; Agpt.
CC DR InterPro; IPR002181; Fibrinogen_C.
CC DR Pfam; PF00147; Fibrinogen_C.1.
CC DR SMART; SM00186; FBG; 1.
CC DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC KW Glycoprotein; Coiled coil; Signal.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 498 ANGIOPOIETIN-1.
CC FT DOMAIN 81 119 COILED COIL (POTENTIAL).
CC FT DOMAIN 153 261 COILED COIL (POTENTIAL).
CC FT DOMAIN 284 498 FIBRINOGEN C-TERMINAL.
CC FT CARBOHYD 92 92 N-LINKED (GLCNAc . . .) (POTENTIAL).
CC FT CARBOHYD 122 122 N-LINKED (GLCNAc . . .) (POTENTIAL).
CC FT CARBOHYD 154 154 N-LINKED (GLCNAc . . .) (POTENTIAL).
CC FT CARBOHYD 243 243 N-LINKED (GLCNAc . . .) (POTENTIAL).
CC FT CARBOHYD 295 295 N-LINKED (GLCNAc . . .) (POTENTIAL).
CC SQ SEQUENCE 498 AA; 57505 MW; 285B4DEC2260D800 CRC64;

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OY 315 LVNGSVSCSHLHKKTTGWMECECLANGTHHS---GKLATGTGLOMTWTKNSPV 370
Db 442 MLTG-----GWMFPACGSPNLNGMFYTAGQNGHGL--NGIKMHFF--KGPSY 484
OY 371 KIKSVSMKIR 380
Db 485 SLRSTTMHIR 494
RESULT 10
AGP2_HUMAN
ID AGP2_HUMAN STANDARD: PRT: 496 AA.
AC 015123; Q9NRR7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; Pubmed=9248496;
RA Matsoukierre P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziejewski C., Compton D., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis.";
RL Science 277:55-60(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=umbilical vein endothelial cells;
RX MEDLINE=20309815; Pubmed=10766762;
RA Kim I., Kim J.-H., Ryu Y.S., Jung S.H., Nah J.J., Koh G.Y.;
RT "Characterization and expression of a novel alternatively spliced
RT human angiopoietin-2.";
RL J. Biol. Chem. 275:18550-18556(2000).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND CONTRACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
CC EMBL, AF004327; AAB63190.1; -
CC EMBL, AF187858; AAF76526.1; -
CC HSSP: P02671; 1FZD.
CC MIM: 601922; -
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; Fibrinogen_C; 1.
CC SMART: SM00186; FBG; 1.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC GlycoProtein: Coiled coil; Signal; Alternative splicing.
CC SIGNAL 1 16 POTENTIAL.
CC CHAIN 17 496 ANGIOPOIETIN-2.

```

FT	DOMAIN	130	256	COILED COIL (POTENTIAL).
FT	DNAIN	180	496	FIBRINOGEN C-TERMINAL.
FT	CARBOHYD	89	89	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	119	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	240	240	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	304	304	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	97	148	MISSING (IN ISOFORM 2).
SO	SEQUENCE	496 AA;	56919 MW;	5642A58847A7385C CRC64;

Query Match	Best Local Similarity	18.1%;	Score 381.5;	DB 1;	Length 496;
Matches 110;	Conservative 73;	Mismatches 138;	Indels 97;	Gaps 16;	

OY	23	VQGNVCVHHSTDDSVVNIYEDGNSNADDESKSNTYCKEDCEESCDYKTKI----	TDEE----	75
Db	112	IQNNVQNOT-----AVMIEIGTNLLNOT-----	AEGTRKLTDVEAOQLNQTRELOL	160
OY	76	-KHMFACRN-LQNSIYSYRSTKTL-----	LRNMDECOASL	109
Db	161	LEHSLSTKLEKQILIDQSEIKKLODKNSFLEKYLAMEDKHIILOLSIKKEKDOQLVLY	220	
OY	110	DYLSNQVVELMNRVLLLT--TEVFRKQ-----	LDPEHPRVQSH	146
Db	221	SKQNSIIIELEKRIATAYVNNVSLQKOOHDLMETVNNLLTMNSTNSAKDPVAREEQIS	280	
OY	147	GLDQDIDITDGSYVKTPTSGLYIIHPREGSYFEFVCEMDYDGSGWTYQIRITDIDFQ	206	
Db	261	FRDCAEVRS-----GHTNGITLTLPFNPSTEDIKAYCDEAGGWTIIQREDESDVQK	336	
OY	207	RIMCDYLDGFGDLGCEFWLGAKIFITYNOKTSMFLYVALESDDPTLAVASYDNFWLED	266	
Db	337	RTWKYEKYKGFQSPSEYEWLMEFVQSOLTNOQR--YVLKIHLMEDWGNEASYLHEFPLSS	394	
OY	267	ETRFKFMHLGRRSGNAGDAFRGLKEDDNQMANPSTSDVDNDGCRPACLVNQSVKSCSH	326	
Db	395	BELNRIHILKGLGTAGAKI-----SISIPGNDPSTKDDNDKC-----	ICKCSQ	439
OY	327	LHNKTGMWFNEECGLANLNGIIHH-----	FSGKLLATSIOMGTWTRKNSPVKIKSVSKIR	380
Db	440	MLT-GGMWFEDACGPNLGMYYPAQONNTNKF--NGIKWYV--	KCSGSLKATYTMWIR	492

RESULT 11	FIBB_HUMAN	STANDARD:	PRT:	491 AA.
ID	FIBB_HUMAN			
AC	P02675;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].			
GN	FGB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
CC	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91344740; PubMed=2102623;			
RA	Chung D.W., Harris J.E., Davie E.W.;			
RT	"Nucleotide sequences of the three genes coding for human			
RL	fibrinogen.";			
RN	Adv. Exp. Med. Biol. 281:39-48(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83283433; PubMed=6688356;			
RA	Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;			
RT	"Characterization of complementary deoxyribonucleic acid and genomic			
RL	deoxyribonucleic acid for the beta chain of human fibrinogen.";			
RN	Biochemistry 22:3244-3250(1983).			
RN	[3]			

RP SEQUENCE FROM N.A.
 RA Chung D.W., Harris J.E., Davie E.W.;
 RT "Nucleotide sequences of the three genes coding for human
 RT fibrinogen.";
 RL (in) Liu C.Y., Chien S. (eds.);
 RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
 RL Plenum Press, New York (1991).
 RN [4]
 RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
 RA Henschel A., Lottspeich F., Southan C., Topfer-Petersen E.;
 RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
 RT structural variants.";
 RL (in) Peeters H. (eds.);
 RL Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
 RL Pergamon Press, Oxford (1980).
 RN [5]
 RP SEQUENCE OF 31-491.
 RX MEDLINE=79124640; PubMed=420779;
 RA Walt K.W.K., Takagi T., Doolittle R.F.;
 RT "Amino acid sequence of the beta chain of human fibrinogen.";
 RL Biochemistry 18:68-76(1979).
 RN [6]
 RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
 RX MEDLINE=76225080; PubMed=936108;
 RA Blomback B., Hessel B., Hogg D.;
 RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
 RL Thromb. Res. 8:639-658(1976).
 RN [7]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87146483; PubMed=3029722;
 RA Huber P., Delmon J., Courtois G., Laurent M., Assouline Z.,
 RA Marguerie G.;
 RT "Characterization of the 5'-flanking region for the human fibrinogen
 RT beta gene.";
 RL Nucleic Acids Res. 15:1615-1625(1987).
 RN [8]
 RP SEQUENCE OF 31-44.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hanton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 RN [9]
 RP REVIEW, AND DISULFIDE BONDS.
 RX MEDLINE=83254370; PubMed=6575689;
 RA Henschel A., Lottspeich F., Kehl M., Southan C.;
 RT "Covalent structure of fibrinogen.";
 RL Ann. N.Y. Acad. Sci. 408:28-43(1983).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=77245999; PubMed=891553;
 RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
 RT "Primary structure of human fibrinogen. Characterization of
 RT disulfide-containing cyanogen-bromide fragments.";
 RL Eur. J. Biochem. 77:595-610(1977).
 RN [11]
 RP DISULFIDE BONDS.
 RA Doolittle R.F., Takagi T., Walt K.W.K., Bouma H. III, Cottrell B.A.,
 RA Cassman K.G., Goldbaum D.M., Doolittle L.R., Friesner S.J.;
 RT "The structures of fibrinogen and fibrin.";
 RL (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
 RL Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
 RL Pergamon Press, New York (1978).
 RN [12]
 RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
 RX MEDLINE=84305751; PubMed=6383194;
 RA Doolittle R.F.;
 RT "Fibrinogen and fibrin.";
 RL Annu. Rev. Biochem. 53:195-229(1984).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
 RX MEDLINE=97472408; PubMed=933233;
 RA Spraggon G., Everse S.J., Doolittle R.F.;
 RT "Crystal structures of fragment D from human fibrinogen and its

RT crosslinked counterpart from fibrin.";
 RL Nature 389:455-462(1997).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
 RX MEDLINE=98292395; PubMed=9628725;
 RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
 RT "Crystal structure of fragment double-D from human fibrin with two
 RT different bound ligands.";
 RL Biochemistry 37:8637-8642(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=99175089; PubMed=10074346;
 RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
 RT "Conformational changes in fragments D and double-D from human
 RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
 RL Biochemistry 38:2941-2946(1999).
 RN [16]
 RP VARIANT BALTIMORE-2.
 RX MEDLINE=89058942; PubMed=3194892;
 RA Schmelzer C.H., Ebert R.F., Bell W.R.;
 RT "A polymorphism at B beta 448 of fibrinogen identified during
 RT structural studies of fibrinogen Baltimore II.";
 RL Thromb. Res. 52:173-177(1988).
 RN [17]
 RP VARIANT ISE.
 RX MEDLINE=91208409; PubMed=2018836;
 RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
 RA Asakura S., Shirakawa S.;
 RT "A new congenital abnormal fibrinogen Ise characterized by the
 RT replacement of B beta glycine-15 by cysteine.";
 RL Blood 77:1958-1963(1991).
 RN [18]
 RP VARIANT NAPLES.
 RX MEDLINE=92340664; PubMed=1634610;
 RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
 RT "Molecular basis of fibrinogen Naples associated with defective
 RT thrombin binding and thrombophilia. Homozygous substitution of B beta
 RT 68 Ala->Thr.";
 RL J. Clin. Invest. 90:238-244(1992).
 RN [19]
 RP VARIANTS IJMUIDEN AND NIJMEGEN.
 RX MEDLINE=92228809; PubMed=1565641;
 RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
 RA Kerst A.F.J.A., Lord S.T.;
 RT "Abnormal fibrinogens IJmuiden (B beta Arg14->Cys) and Nijmegen (B
 RT beta Arg44->Cys) form disulfide-linked fibrinogen-albumin
 RT complexes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
 RN [20]
 RP VARIANT NEW YORK-1.
 RX MEDLINE=85157605; PubMed=3156856;
 RA Liu C.Y., Koehn J.A., Morgan F.J.;
 RT "Characterization of fibrinogen New York 1. A dysfunctional
 RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
 RT exon 2 of the gene.";
 RL J. Biol. Chem. 260:4390-4396(1985).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLIMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
 CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -1- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS

CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J00129; AAA52429.1; -
DR EMBL: J00131; AAA98115.1; -
DR EMBL: J00130; AAA98115.1; JOINED.
DR EMBL: J00132; AAA98116.1; -
DR EMBL: J00133; -; NOT_ANNOTATED_CDS.
DR EMBL: X05018; CAA28674.1; -
DR EMBL: M64983; AAA18024.2; -
DR EMBL: M26877; AAA52445.1; -
DR EMBL: M26876; AAA52445.1; JOINED.
DR PIR: B43568; FGHUB.
DR PDB: 1FZA; 03-DEC-97.
DR PDB: 1FZB; 03-DEC-97.
DR PDB: 1FZC; 14-OCT-98.
DR PDB: 1FZE; 08-JUN-99.
DR PDB: 1FZF; 08-JUN-99.
DR PDB: 1FZG; 08-JUN-99.

Query Match 17.8%; Score 375.5; DB 1; Length 491;
Best Local Similarity 26.6%; Pred. No. 1,8e-22;

Matches 118; Conservative 56; Mismatches 142; Indels 127; Gaps 17;

OY 25 GNCVHSHSTDSVYNIIVEDGNSNAKDESKSNDTYCKEDCEESCVKTKITREKHFMCRNLQ 84
DB 93 GCCLHADPLGLV-----CPGCOLGEXLLQOE-----RPFR 124
OY 65 NSI-----VSYTRSK-----KLRRMMDQASLDYLSNOVELMN-----121
DB 125 NSVDELNNNEAVSQTSSSFQYMYLLDLQWQKQKQVNDENYNEVSSELEKHQLYTD 184
OY 122 -----RVLLTTEVFRKQLDPP-----HRRYOSHGLDCTD 152
DB 165 ETVNSNIPNLRLVLSILENLSKIQKLESDVSAQMEYCRTPCTYSNCPVYS-GKECEE 243
OY 153 IKDTGVSATKTPSGLYIHPGESSYRFEVYCDMDYRGCGWTVIQKRIDGIDDFQRLMCDY 212
DB 244 IIRKGGGT-----SEMYLIQPDSSVKKPRVYCDMNTENGWTVIQNRQDSYDFGKRMDDY 299
OY 213 LDGFGD-----LLGEFWLGKRIFYIVNOKNTSFMLYALAESEDDTLAYASD 260
DB 300 KQGFENVATNTDGNKYGCGIPGYWLGNDISQLTRNGPTE--LLIEMEDWKGDKYKAHYG 357
OY 261 NFWLEDETFEFKMLGRVSGNAGDAFRG-----LKKEDN-----QNAPEFSTSDVNDGCRP 312
DB 358 GFTYQNEANKYQISVKNKYGSTAGNMLMDQASOLMGENTRTHTHNGFEFTYRDNDG----414
OY 313 ACLVNGQSVKSCSHLHNTGMPFNECCGLANLNGIHHSFKL-----LATGIQWGTWT 364
DB 415 -WLTSDPKQCSK-EDGGGWYNRCHANPNRGYRWGQYWDMAKHGTDGQVYVMNN-470
OY 365 KNSPVKTIKSVSMKTRRMNPFY 387
DB 471 -KGSWYSMKRMSMKIR---PFF 488

RESULT 12
AGP2_BOVIN
ID AGP2_BOVIN STANDARD: PRT: 375 AA.
AC 077802; Q9TJKO;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Angiotensin-2 (ANG-2) (Fragment).
GN ANGPT2 OR ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE:99054348; PubMed:9840613;
RA Goede V., Schmidt T., Kimmig S., Kozian D., Augustin H.G.;
RT "Analysis of blood vessel maturation processes during cyclic ovarian
RT angiogenesis."
RL Lab. Invest. 78:1385-1394(1998).
RN (2)
RP SEQUENCE OF 219-355 FROM N.A.
RC TISSUE-Adrenal cortex;
RX MEDLINE:98451564; PubMed:9776732;
RA Mandriota S.J., Pepper M.S.;
RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular
RT endothelial cells by cytokines and hypoxia."
RL Circ. Res. 83:852-859(1998).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOTENSIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG-2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: FOUND TO BE EXPRESSED THROUGHOUT THE OVARIAN
CC CYCLE. OVEREXPRESSED DURING LUTEOLYSIS, THIS COULD REFLECT THE
CC REGRESSION OF CAPILLARIES THAT HAD DEVELOPED PERICYTE CONTACT IN
CC THE MIDSTAGE CORPUS LUTEUM.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF094699; AAC62490.1; -
DR EMBL: AF032924; AAC78285.1; -
DR HSSP: P02671; 1FZD
DR InterPro: IPR002181; Fibrinogen_C.
DR Pfam: PF00147; Fibrinogen_C; 1.
DR SMART: SM00186; FBG; 1.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Glycoprotein; Coiled coil.
FT NON_TER 1 1
FT DOMAIN 10 138 COILED COIL (POTENTIAL).
FT DOBAYD 159 375 FIBRINOGEN C-TERMINAL.
FT CAROHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 272 272 S -> L (IN REF. 2).
SQ SEQUENCE 375 AA; 42761 MW; 6F086C4A5C80050A CRC64;

Query Match 17.8%; Score 375; DB 1; Length 375;
Best Local Similarity 30.2%; Pred. No. 1.4e-22;

Matches 112; Conservative 57; Mismatches 136; Indels 66; Gaps 15;

OY 31 STDSVYNIIVEDGNSNAKDESKSNDTYCKE--DCEESCVKTKITREKHFM--CNLONS 86
DB 46 STNLEKQILDQTSLSKLDKNSFLKKVLDMEKHIVQLRSIKREKQDQVLVSKONS 105

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RESULT 13
AGP2_MOUSE
ID AGP2_MOUSE STANDARD: PRT: 496 AA.
AC O35608;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2 OR AGPT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=97349327; Pubmed=9204896;
RA Mazonpiere P.C., Surt C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziszewski C., Compton D.L., McClain J., Aldrich T.H.,
RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis."
RL Science 277:55-60(1997).
CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTRACTS MAY
CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
CC ANGIOGENIC SIGNAL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY AT SITES OF VASCULAR
CC REMODELING.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF004326; AAB63189.1; -
CC HSSP: P02671; 1FZD
CC MGD: MGI:1202890; Agpt2.
CC InterPro: IPR002181; Fibrinogen.C.

```

Query Match	17.8%;	Score 374.5;	DB 1;	Length 496;
Best Local Similarity	25.5%;	Pred. No. 2.2e-22;		
Matches 110;	Conservative 72;	Mismatches 125;	Indels 125;	Gaps 16

	RESULT	14
FTBB_RAT		
ID	FTBB_RAT	STANDARD; PRT; 479 AA.
AC	P14480.	
DT	01-JAN-1990 (Rel. 13, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].	
CN	FCB	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Cranialta; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;	
RX	MEDLINE=95143386; Pubmed=7841303;	
RA	Courtney M.A., Bunce L.A., Neroni L.A., Stimpson-Haidaris P.J.;	
RT	"Cloning of the complete coding sequence of rat fibrinogen B beta	

RT chain cDNA: interspecies conservation of fibrin beta 15-42 primary structure.";
 RL Blood Coagul. Fibrinolysis 5:487-496(1994).
 RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=84194000; PubMed=6232608;
 RA Fowkes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.;
 RT "Potential basis for regulation of the coordinately expressed
 RL fibrinogen genes: homology in the 5' flanking regions.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316(1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RX MEDLINE=89378771; PubMed=2673932;
 RA Eastman E.M., Gillula N.B.;
 RT "Cloning and characterization of a cDNA for the B beta chain of rat
 RL fibrinogen: evolutionary conservation of translated and
 RT 3'-untranslated sequences.";
 RL Gene 79:151-158(1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.
 RX STRAIN=WISTAR; TISSUE=Liver;
 RX MEDLINE=87134033; PubMed=3817019;
 RA Sobczak J., Lotli A.-M., Taroux P., Duguet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 RL liver regeneration.";
 RL Exp. Cell Res. 169:47-56(1987).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
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 CC -----
 DR EMBL; U05675; AAA64866.1; -;
 DR EMBL; M27220; AAA41160.1; -;
 DR EMBL; K01336; AAA98625.1; -;
 DR EMBL; M35602; AAA41159.1; -;
 DR PIR; A05299; A05299;
 DR PIR; PE0010; PE0010;
 DR HSBP; P02673; IPIZE.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR SMART; PF00147; fibrinogen_C; 1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM BLOOD coagulation; Plasma; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
 FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
 FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
 FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
 FT DISULFID 219 304 (BY SIMILARITY).
 FT DISULFID 229 258 (BY SIMILARITY).
 FT DISULFID 412 425 BY SIMILARITY.
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
 FT CONFLICT 439 439 L -> Q (IN REF. 5).
 FT CONFLICT 441 441 S -> T (IN REF. 5).
 FT CONFLICT 445 445 S -> A (IN REF. 5).
 FT CONFLICT 467 467 R -> K (IN REF. 5).
 FT CONFLICT 475 475 V -> F (IN REF. 5).
 SQ SEQUENCE 479 AA: 54303 MW: EC8CDB77C3B0EC0 CRC64;
 Query Match 17.8%; Score 373.5; DB 1; Length 479;
 Best Local Similarity 27.2%; Pred. No. 2,5e-22;
 Matches 119; Conservative 49; Mismatches 149; Indels 121; Gaps 15;
 Db 25 GNCVHSHDSSVNVIVEDGSAKDESKNDYVKEDESCDVKTKITREKHPCRNQ 84
 81 GCVHGDGDMGVL-----CATGCELRLQTLNHE-----RPIK 112
 QY NSIV-----SYTRSTKKLLNNMDEQASLDYLSNQVNE----- 118
 Db 113 NSIAELNSINSVETSSVTFOYLTLLKDMKKQAOYKDNENYINEXSSILEDQKLYID 172
 QY 119 -----LMNRVLTLTEVERKQD-----PPHAPVQSH-----GLDCTDI 153
 Db 173 ETVNDNITPLNRLVRLSLIEDLRSKMQLSDISAQTECHTPCYVNCIPIYVSGKECEI 232
 QY 154 KDTIGSVKTPSGLYIHPESSYPFEVYCDMDYRGGMVYIQRIDGIIDFQRLMCDYL 213
 Db 223 IRKGSET-----SEWLIIDPTSSKRYVCDMKTEENGWFIQONQDSYDFGRKMDPK 288
 QY 214 DGFGD-----LLGFEVLGLKRTFYIVNKNISFPLLYALBESDITLAVASYDN 261
 Db 289 KGFGIATNEDTKKYCGLPGEYWLGNDKISQITRIGPE--LLEMEWKGDKYKAHGG 346
 QY 262 FWLEDETRFFKMHILGRYSNGADAF---RLKREDN---QNAPEFSTDVDNDGCRPA 313
 Db 347 FTYQTEANKKYQSVNKKYGTAGNMLMEGASQLVGNRRTITNGFFTYRDNDG----- 402
 QY 314 CLVNGSVKSCSHLHNTKGMFNECGLANLNGIHFSKLV-----LATGIQGTWTK 365
 Db 403 -WVTIDPRKQCSK-EDGGWYNNRCHAMPNGRYWGLYSWDSKSHGTDDGVVMMNV-- 458
 QY 366 NNSPVKIKSVSMKIRMY 383
 Db 459 KGSWISMRMSKTRPVF 476
 RESULT 15
 FTBB_CHICK
 ID FTBB_CHICK STANDARD: PRT: 463 AA.
 AC 002020;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
 DE (Fragment).
 GN FGB.
 OS Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
 RX MEDLINE=91182745; PubMed=2009266;
 RA Weissbach L., Odoux C., Procyk R., Grieninger G.;
 RT "The beta chain of chicken fibrinogen contains an atypical thrombin
 RL cleavage site.";
 RL Biochemistry 30:3290-3294(1991).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

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